

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 12:21:16 ; Search time 1081.59 Seconds
(without alignments)
2822.391 Million cell updates/sec

Title: US-10-820-777-1

Perfect score: 63

Sequence: 1 atgatgtcctttgtctctc.....atgcaccaccaggtgtaac 63

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	92.1	283	4 AB034967	AB034967 Bos tauru
2	58	92.1	283	4 AB040058	AB040058 Ovis arie
3	58	92.1	283	4 AB040059	AB040059 Bos tauru
4	58	92.1	283	4 AB040060	AB040060 Bos tauru
5	58	92.1	283	4 AB040061	AB040061 Bos tauru
6	58	92.1	295	4 AB034981	AB034981 Bos tauru
7	58	92.1	703	4 BOVLACTBA	M18780 Bovine alph
8	58	92.1	723	4 CALACA	X06367 Ovine mRNA
9	58	92.1	724	4 BOVALACT	J05147 Bovine alph
10	58	92.1	1855	4 AB052168	AB052168 Ovis arie
11	58	92.1	1868	4 AB052163	AB052163 Bos tauru
12	58	92.1	1870	4 AB052164	AB052164 Bos tauru
13	58	92.1	1870	4 AB052166	AB052166 Bos tauru
14	58	92.1	1871	4 AB052167	AB052167 Bos tauru
15	58	92.1	1896	4 AB052165	AB052165 Bos tauru
16	58	92.1	2044	4 BOVLACTAUB	M90645 Cow alpha-1
17	58	92.1	2044	6 AR066426	AR066426 Sequence
18	58	92.1	2784	4 AF194373	AF194373 Bubalus a
19	58	92.1	2999	4 AF194372	AF194372 Bos grunn

c	20	58	92.1	169904	2	AC150961	AC150961 Bos tauru
	21	56.4	89.5	133	4	AY726609S1	AY726609 Bubalus b
	22	56.4	89.5	133	4	AY726610S1	AY726610 Bubalus b
	23	56.4	89.5	133	4	AY726611S1	AY726611 Bubalus b
	24	56.4	89.5	708	4	CHLACTAR	X05149 Goat mRNA f
	25	56.4	89.5	2819	4	AF249896	AF249896 Bos tauru
	26	56.4	89.5	3090	4	BTALACTA	X06366 Bovine gene
	27	56.4	89.5	3153	4	GOTALAL	M63868 C.hircus al
	28	56.4	89.5	4532	6	AR452811	AR452811 Sequence
	29	56	88.9	5691	6	AX359937	AX359937 Sequence
	30	56	88.9	5691	6	AX382151	AX382151 Sequence
	31	54.8	87.0	133	4	AY726612S1	AY726612 Bubalus b
	32	51.8	82.2	4207	6	AX359930	AX359930 Sequence
	33	51.8	82.2	4207	6	AX382144	AX382144 Sequence
	34	51.8	82.2	4210	6	AX359931	AX359931 Sequence
	35	51.8	82.2	4210	6	AX382145	AX382145 Sequence
	36	51.8	82.2	5732	6	AX359932	AX359932 Sequence
	37	51.8	82.2	5732	6	AX382146	AX382146 Sequence
	38	51.8	82.2	9183	6	AX359933	AX359933 Sequence
	39	51.8	82.2	9183	6	AX382147	AX382147 Sequence
	40	51.6	81.9	680	6	AX359929	AX359929 Sequence
	41	51.6	81.9	680	6	AX382143	AX382143 Sequence
	42	51.6	81.9	5711	6	AX359934	AX359934 Sequence
	43	51.6	81.9	5711	6	AX382148	AX382148 Sequence
	44	51.6	81.9	6255	6	AX359939	AX359939 Sequence
	45	51.6	81.9	6255	6	AX382153	AX382153 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AB034967 Bos taurus gene for alpha lactalbumin, partial cds.
DEFINITION Bos taurus gene for alpha lactalbumin, partial cds.
ACCESSION AB034967
VERSION AB034967.1 GI:6451686
KEYWORDS alpha lactalbumin.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1
AUTHORS Yamamoto,N.
TITLE Bovine alpha-lactalbumin gene
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 283)
AUTHORS Yamamoto,N.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-1999) Naoyuki Yamamoto, National Agricultural Research Organization, National Agricultural Research Center for

Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Htsujigoka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
(E-mail:nymmt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)

FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 58
Db 95 ATGATGTCCTTTGCTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 152

RESULT 5
AB040061
LOCUS      283 bp DNA linear MAM 30-MAY-2002
DEFINITION Bos taurus a-LACTA gene for alpha-lactalbumin, partial cds,
ACCESSION AB040061
VERSION    1 GI:7288123
KEYWORDS   a-LACTA; alpha-lactalbumin.
SOURCE     Bos taurus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE
1 Yamamoto,N. and Moritsu,Y.
AUTHORS    Bovine gene for alpha lactalbumin, partial cds
TITLE      Published Only in Database (2000)
JOURNAL
REFERENCE   2 (bases 1 to 283)
AUTHORS    Yamamoto,N. and Moritsu,Y.
TITLE      Direct Submission
JOURNAL    Submitted (13-MAR-2000) Naoyuki Yamamoto, National Agricultural
Research Organization, National Agricultural Research Center for
Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Hitsujioka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
(E-mail:nymmt@affrc.go.jp, tel:81-11-857-9270, fax:81-11-859-2178)

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/dev_stage="adult"
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ORIGIN
Query Match          92.1%; Score 58; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 58
Db 95 ATGATGTCCTTTGCTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 152

RESULT 6
AB034981
LOCUS      295 bp DNA linear MAM 30-MAY-2002
DEFINITION Bos taurus gene for alpha lactalbumin, partial cds.
ACCESSION AB034981
VERSION    1 GI:6451693
KEYWORDS   alpha lactalbumin.
SOURCE     Bos taurus (cow)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE
1 Yamamoto,N.
AUTHORS    Bovine alpha-lactalbumin gene
TITLE      Published Only in Database (1999)
JOURNAL
REFERENCE   2 (bases 1 to 295)
AUTHORS    Yamamoto,N.
TITLE      Direct Submission
JOURNAL    Submitted (15-NOV-1999) Naoyuki Yamamoto, National Agricultural
Research Organization, National Agricultural Research Center for
Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Hitsujioka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
(E-mail:nymmt@affrc.go.jp, tel:81-11-857-9270, fax:81-11-859-2178)

FEATURES
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/protein_id="BAA86914.1"
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Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 103 ATGATGTCCTTTGCTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 160

RESULT 7
BOVLACTBA
LOCUS      703 bp mRNA linear MAM 27-APR-1993
DEFINITION Bovine alpha-lactalbumin mRNA, complete cds.
ACCESSION M18780
VERSION    M18780.1 GI:163282
KEYWORDS   lactalbumin.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus

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/protein_id="BAA92834.1"
/db_xref="GI:7288122"
/translation="MMSFVSLLLVGLFHATQAEQLTKCEVFRELKDLKGYGVSLPE
CEFPAILLCPIIHLHSPF"

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Query Match          92.1%; Score 58; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 58
Db 95 ATGATGTCCTTTGCTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 152

RESULT 6
AB034981
LOCUS      295 bp DNA linear MAM 30-MAY-2002
DEFINITION Bos taurus gene for alpha lactalbumin, partial cds.
ACCESSION AB034981
VERSION    1 GI:6451693
KEYWORDS   alpha lactalbumin.
SOURCE     Bos taurus (cow)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE
1 Yamamoto,N.
AUTHORS    Bovine alpha-lactalbumin gene
TITLE      Published Only in Database (1999)
JOURNAL
REFERENCE   2 (bases 1 to 295)
AUTHORS    Yamamoto,N.
TITLE      Direct Submission
JOURNAL    Submitted (15-NOV-1999) Naoyuki Yamamoto, National Agricultural
Research Organization, National Agricultural Research Center for
Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Hitsujioka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
(E-mail:nymmt@affrc.go.jp, tel:81-11-857-9270, fax:81-11-859-2178)

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ORIGIN
Query Match          92.1%; Score 58; DB 4; Length 295;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 58
Db 103 ATGATGTCCTTTGCTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 160

RESULT 7
BOVLACTBA
LOCUS      703 bp mRNA linear MAM 27-APR-1993
DEFINITION Bovine alpha-lactalbumin mRNA, complete cds.
ACCESSION M18780
VERSION    M18780.1 GI:163282
KEYWORDS   lactalbumin.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
AUTHORS 1 (bases 1 to 703)
TITLE Molecular cloning and nucleotide sequence of a bovine
alpha-lactalbumin cDNA
JOURNAL Gene 61 (1), 119-122 (1987)
MEDLINE 88167838
PUBMED 3443304
COMMENT Original source text: Bovine (strain Holstein) lactating mammary
gland, cDNA to mRNA, clone pB-alpha-La5
Draft entry and computer-readable form of sequence [1] kindly
provided by W.L.Hurley 25-MAR-1988.
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9..437
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66..434
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Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 9 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 66
RESULT 8
OALACA OALACA 723 bp mRNA linear MAM 23-FEB-1995
LOCUS Ovine mRNA for alpha-lactalbumin.
DEFINITION X06367
ACCESSION X06367
VERSION alpha-lactalbumin; lactalbumin.
KEYWORDS Ovis aries (sheep)
SOURCE Ovis aries
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
1 (bases 1 to 723)
Gaye,P., Hue-Delahaie,D., Mercier,J.C., Soulier,S., Vilotte,J.L.
and Furet,J.P.
TITLE Complete nucleotide sequence of ovine alpha-lactalbumin mRNA
JOURNAL Biochimie 69 (6-7), 601-608 (1987)
MEDLINE 88078101
PUBMED 3120794
COMMENT Data kindly reviewed (26-SEP-1988) by GAYE P.
FEATURES
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CDS

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Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 27 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 84
RESULT 9
BOVALACT BOVALACT 724 bp mRNA linear MAM 26-APR-1993
LOCUS Bovine alpha-lactalbumin mRNA, complete cds.
DEFINITION J05147
ACCESSION J05147
VERSION alpha-lactalbumin; milk protein; regulatory protein.
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 724)
Wang,M., Scott,W.A., Rao,K.R., Udev,J., Conner,G.E. and Brew,K.
Recombinant bovine alpha-lactalbumin obtained by limited
proteolysis of a fusion protein expressed at high levels in
Escherichia coli
J. Biol. Chem. 264 (35), 21116-21121 (1989)
JOURNAL 90078209
MEDLINE 2687274
PUBMED
COMMENT Original source text: Bovine (adult) mammary, cDNA to mRNA,
Library of Okayama and Berg).
Draft entry and computer-readable sequence for [1] kindly submitted
by K.Brew, 18-NOV-1989.
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 28 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 85

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RESULT 10
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LOCUS
DEFINITION      Ovis aries gene for alpha lactalbumin, complete cds,
                  strain:Corriedale.
ACCESSION      AB052168
VERSION
KEYWORDS
SOURCE
ORGANISM
Ovis aries (sheep)
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
JOURNAL
AUTHORS
TITLE
JOURNAL
JOURNAL
Yamamoto, N.
Submitted (05-DEC-2000) Naoyuki Yamamoto, National Agricultural
Research Organization, National Agricultural Research Center for
Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Hitsujiigaoka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
(E-mail:nyamt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)
FEATURES
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/product="alpha lactalbumin"
/protein_id="BAB18926.1"
/db_xref="GI:11610599"
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ORIGIN
Query Match      92.1%; Score 58; DB 4; Length 1855;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGTCCTTTGCTCTGCTGCTAGGATCCTATTCATGCGACCCAGGCTG 58
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DB 95 ATGATGTCCTTTGCTCTGCTGCTAGGATCCTATTCATGCGACCCAGGCTG 152
|||||

RESULT 11
AB052163          1868 bp      DNA      linear      MAM 30-MAY-2002
LOCUS
DEFINITION      Bos taurus gene for alpha lactalbumin, complete cds, strain:Jersey.
ACCESSION      AB052163
VERSION
KEYWORDS
SOURCE
ORGANISM
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
JOURNAL
Yamamoto, N.
Submitted (05-DEC-2000) Naoyuki Yamamoto, National Agricultural
Research Organization, National Agricultural Research Center for
Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Hitsujiigaoka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
(E-mail:nyamt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)
FEATURES
source
1..1868
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGTCCTTTGCTCTGCTGCTAGGATCCTATTCATGCGACCCAGGCTG 58
|||||
DB 95 ATGATGTCCTTTGCTCTGCTGCTAGGATCCTATTCATGCGACCCAGGCTG 152
|||||

RESULT 12
AB052164          1870 bp      DNA      linear      MAM 30-MAY-2002
LOCUS
DEFINITION      Bos taurus gene for alpha lactalbumin, complete cds,
                  strain:Hereford.
ACCESSION      AB052164
VERSION
KEYWORDS
SOURCE
ORGANISM
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
JOURNAL
Yamamoto, N.
Submitted (05-DEC-2000) Naoyuki Yamamoto, National Agricultural
Research Organization, National Agricultural Research Center for
Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
Hitsujiigaoka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
(E-mail:nyamt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGTCCTTTGCTCTGCTGCTAGGATCCTATTCATGCGACCCAGGCTG 58
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ORIGIN

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Query Match 92.1%; Score 58; DB 4; Length 1870;
 Best Local Similarity 100.0%; Pred. No. 2.7e-10; Indels 0; Gaps 0;
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Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 58
 |||||
 Db 96 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 153
 |||||

RESULT 13
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 LOCUS
 DEFINITION Bos taurus gene for alpha lactalbumin, complete cds,
 strain:Holstein.
 ACCESSION AB052166
 VERSION AB052166.1 GI:11610594
 KEYWORDS
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1
 AUTHORS Yamamoto,N.
 TITLE Bos taurus alpha lactalbumin gene
 JOURNAL Published Only in Database (2000)
 REFERENCE 2 (bases 1 to 1870)
 AUTHORS Yamamoto,N.
 TITLE Direct Submission
 JOURNAL Submitted (05-DEC-2000) Naoyuki Yamamoto, National Agricultural
 Research Organization, National Agricultural Research Center for
 Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
 Hitsujigaoka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
 (E-mail:nymmt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)

FEATURES
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ORIGIN

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Query Match 92.1%; Score 58; DB 4; Length 1870;
 Best Local Similarity 100.0%; Pred. No. 2.7e-10; Indels 0; Gaps 0;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 58
 |||||
 Db 96 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 153
 |||||

RESULT 14
 AB052167
 LOCUS
 DEFINITION Bos taurus gene for alpah lactalbumin, complete cds,
 strain:Japanese black.
 ACCESSION AB052167
 VERSION AB052167.1 GI:11610596
 KEYWORDS
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1
 AUTHORS Yamamoto,N.
 TITLE Bos taurus alpha lactalbumin gene
 JOURNAL Published Only in Database (2000)
 REFERENCE 2 (bases 1 to 1871)
 AUTHORS Yamamoto,N.
 TITLE Direct Submission
 JOURNAL Submitted (05-DEC-2000) Naoyuki Yamamoto, National Agricultural
 Research Organization, National Agricultural Research Center for
 Hokkaido Region, Laboratory of Animal Breeding and Genetics; 1
 Hitsujigaoka, Toyohira, Sapporo, Hokkaido 062-8555, Japan
 (E-mail:nymmt@affrc.go.jp, Tel:81-11-857-9270, Fax:81-11-859-2178)

FEATURES
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 /organism="Bos taurus"
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ORIGIN

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Query Match 92.1%; Score 58; DB 4; Length 1871;
Best Local Similarity 100.0%; Pred. No. 2.7e-10; Indels 0; Gaps 0;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 58
|||||
Db 113 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 170
|||||

```

RESULT 15
 AB052165
 LOCUS
 DEFINITION Bos taurus gene for alpha lactalbumin, complete cds, strain:Angus.
 ACCESSION AB052165
 VERSION AB052165.1 GI:11610592
 KEYWORDS
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1
 AUTHORS Yamamoto,N.
 TITLE Bos taurus alpha lactalbumin gene
 JOURNAL Published Only in Database (2000)
 REFERENCE 2 (bases 1 to 1896)
 AUTHORS Yamamoto,N.

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XX Unidentified.
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XX FT /label= 5' LTR
XX FT 807..1616
XX FT /*tag= b
XX FT /label= Extended_packaging_region
XX FT 1660..2454
XX FT /*tag= c
XX FT /product= "Neo"
XX FT 1679..1735
XX FT /*tag= d
XX FT /label= EM7_promoter
XX FT 2804..3621
XX FT /*tag= e
XX FT /label= hCMV_promoter
XX FT 3625..3649
XX FT /*tag= f
XX FT /label= aatB1
XX FT 3727..4443
XX FT /*tag= g
XX FT /product= "LL2 LC"
XX FT 4460..4484
XX FT /*tag= h
XX FT /label= attB2
XX FT 4536..5129
XX FT /*tag= i
XX FT /label= 3' LTR
XX FT complement(6425..7285)
XX FT /*tag= j
XX FT /label= AMP
XX WO2003083077-A2.
XX 09-OCT-2003.
XX 28-MAR-2003; 2003WO-US009662.
XX 28-MAR-2002; 2002US-0368808P.
XX 10-APR-2002; 2002US-0371299P.
XX 28-MAR-2003; 2003US-00371299.
XX (GALA-) GALA DESIGN INC.
XX Bremel RD, Bakle K, Imboden M;
XX WPI; 2003-804051/75.
XX P-PSDB; ADE64202, ADE64203.
XX New antibody library comprising cells comprising at least one integrated
XX retroviral vector expressing an antibody light or heavy chain, useful in
XX preparing a composition for diagnosing or treating disorders.
XX Example 1; SEQ ID NO 3; 57pp; English.
XX This invention relates to a new antibody library which comprises at least
XX 100 cells, each of which comprises at least one integrated retroviral
XX vector expressing an antibody light or heavy chain. Antibodies are of
XX increasing importance in human therapy, assay procedures and diagnostic
XX methods and a need exists for efficient methods of generating and
XX screening antibody libraries containing large numbers of antibodies. The
XX antibody library of the invention addresses this need, with the
XX additional advantage of strict control over multiplicity of infection
XX (MOI), and is useful in preparing a composition for diagnosing or
XX treating a wide variety of disorders. The present sequence is the nucleic
XX acid sequence of pBLC-L2LC, a GATEWAY retroviral vector containing DNA
XX encoding the LL2 antibody light chain, which was used in the
XX exemplification of the invention.
XX Sequence 7490 BP; 1764 A; 2041 C; 1894 G; 1791 T; 0 U; 0 Other;
XX
```

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Query Match 89.8%; Score 56.6; DB 10; Length 7490;
Best Local Similarity 93.7%; Pred. No. 7.7e-10;
Matches 59; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGATGTCCTTTGCTCTCTCTGCTGCTAGGCATCCTATTCATGCCACCCAGGCTGTT 60
Db 3727 ATGATGTCCTTTGCTCTCTCTGCTGCTAGGCATCCTATTCATGCCACCCAGGCTGTT 60
Qy 61 AAC 63
Db 3787 ATC 3789
RESULT 8
AAD32015
ID AAD32015 standard; DNA; 4532 BP.
XX AC AAD32015;
XX 29-AUG-2003 (revised)
XX 18-JUN-2002 (first entry)
XX DE Bovine alpha lactalbumin/IGF-I chimeric gene construct.
XX KW Transgenic animal; weight gain; lactase activity; pathogen resistance;
XX KW rotovirus; coronavirus; Escherichia coli; Salmonella; piglet development;
XX KW bovine; porcine; human; insulin-like growth factor I; alpha lactalbumin;
XX KW IGF-I; chimeric; LA; ds.
XX OS Bos sp.
XX OS Sus scrofa.
XX OS Homo sapiens.
XX OS Chimeric.
XX PH Key
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XX FT 1952
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XX FT /note= "Bovine alpha-lactalbumin transcription start
XX FT point"
XX FT 1989..2045
XX FT /*tag= c
XX FT /note= "Bovine alpha-lactalbumin signal peptide coding
XX FT region"
XX FT 2046..2255
XX FT /*tag= d
XX FT /product= "Human/Bovine/Porcine IGF-I protein"
XX FT 2256..2258
XX FT /*tag= e
XX FT /note= "IGF-I stop codon"
XX FT 2259..2340
XX FT /*tag= f
XX FT /number= 1
XX FT /note= "Bovine alpha-lactalbumin 3' end of exon 1"
XX FT partial
XX FT 2341..2661
XX FT /*tag= g
XX FT /number= 1
XX FT /note= "Bovine alpha-lactalbumin intron 1"
XX FT 2662..2820
XX FT /*tag= h
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XX FT 2821..3294
XX FT /*tag= i
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XX FT /note= "Bovine alpha-lactalbumin intron 2"
XX FT 3295..3369
XX FT /*tag= j
XX FT /number= 3
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FT /note= "Bovine alpha-lactalbumin exon 3"
FT 3370. .3873
FT /*tag= k
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FT /note= "Bovine alpha-lactalbumin intron 3"
FT 3874. .4203
FT /*tag= l
FT /number= 4
FT /note= "Bovine alpha-lactalbumin exon 4"
FT 4204. .4532
FT /*tag= m
FT /note= "Bovine alpha-lactalbumin 3' flanking region"
XX
XX WO200214473-A2.
XX
XX 21-FEB-2002.
XX
XX 15-AUG-2001; 2001WO-US025583.
XX
XX 15-AUG-2000; 2000US-0225474P.
XX (UNII ) UNIV ILLINOIS FOUND.
XX
XX Wheeler MB, Donovan SM, Bleck GT, Monaco-Seigel M;
XX WPI; 2002-269186/31.
XX
XX New transgenic animals (e.g. pig) that express an increased milk volume
XX and growth factors in their milk, useful for increasing the weight gain
XX or resistance to pathogens, or improving health in a suckling animal.
XX
XX Claim 10; Fig 3; 67pp; English.
XX
XX The invention relates to transgenic animals (e.g. pig) that express an
XX increased milk volume and growth factors e.g. insulin-like growth factor
XX I (IGF-I) in their milk. The invention also provides transgenic animals
XX with a genome which comprises a heterologous nucleic acid sequence
XX encoding a growth factor and/or alpha-lactalbumin (LA) operably linked to
XX a mammary preferential promoter. The transgenic animals are useful for
XX increasing the amount or volume of growth factor in milk, as well as for
XX increasing the volume of milk. They are also useful in method for
XX increasing the weight gain, intestinal lactase activity, intestinal cell
XX division, intestinal villi length, and resistance to intestinal pathogens
XX (e.g. rotavirus, coronavirus, Escherichia coli or Salmonella) in suckling
XX animals. The transgenic animals are also useful for providing milk to
XX facilitate piglet development, improve health and decrease piglet
XX mortality. The present sequence is bovine alpha lactalbumin-
XX human/bovine/porcine IGF-I chimeric gene construct. (Updated on 29-AUG-
XX 2003 to standardise OS field)
XX
XX SQ Sequence 4532 BP; 1168 A; 983 C; 1014 G; 1367 T; 0 U; 0 Other;
XX
XX Query Match 89.5%; Score 56.4; DB 6; Length 4532;
XX Best Local Similarity 98.3%; Pred. No. 8.1e-10;
XX Matches 57; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTGAGCATCTATTCATGCCACCCAGGCTG 58
XX |||||||
XX Db 1989 ATGATGTCCTTTGCTCTCTGCTCTGCTGAGCATCTATTCATGCCACCCAGGCTG 2046
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XX RESULT 9
XX AAD28313
XX ID AAD28313 standard; DNA; 5691 BP.
XX
XX AC AAD28313;
XX
XX XX
XX DT 07-AUG-2003 (revised)
XX DT 22-APR-2002 (first entry)
XX
XX XX
XX DE Alpha-lactalbumin (LA) YP vector.
XX
XX KW Regulatory element; vector; erythropoietin; growth hormone; insulin;

```

```

KW immunoglobulin; bone morphogenetic protein; interferon; interleukin;
KW superoxide dismutase; T-cell receptor; surface membrane protein; WPRE;
KW viral antigen; transport protein; addressin; regulatory protein; IRES;
KW bovine; alpha-lactalbumin; promoter; ECMV; encephalomyocarditis virus;
KW internal ribosome entry site; moloney murine leukemia virus; MoMuLV;
KW woodchuck mRNA processing enhancer; pre-mRNA processing enhancer; PPE;
KW human; chimeric; ds.
XX
XX Encephalomyocarditis virus.
XX Bos sp.
XX Homo sapiens.
XX Moloney murine leukemia virus.
XX Marmota monax.
XX Yersinia pestis.
XX Unidentified.
XX Chimeric.
XX
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XX /note= "Double mutated PPE sequence"
XX 2403..2459
XX /tag= c
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XX 2460..3137
XX /tag= d
XX /product= "Yersenia pestis heavy chain Fab gene coding
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XX 3167..3742
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XX /note= "WPRE sequence"
XX 5098..5691
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XX /note= "MoMuLV 3' LTR"
XX
XX WO200202783-A2.
XX
XX 10-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US020714.
XX
XX 03-JUL-2000; 2000US-0215851P.
XX
XX (GALA-) GALA DESIGN INC.
XX
XX Bleck GT;
XX
XX WPI; 2002-154749/20.
XX
XX Novel regulatory elements including nucleic acid encoding hybrid alpha-
XX lactalbumin promoter or mutant RNA export element, for expressing one or
XX more proteins e.g. antibodies, pharmaceutical proteins in host cells.
XX
XX Example 1; Fig 14; 151pp; English.
XX
XX The invention relates to novel regulatory elements and vectors for the
XX expression of one or more proteins in a host cell. The invention further

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provides methods of indirectly detecting the expression of a protein of interest, comprising providing the host cell transfected with a vector encoding a polycistronic sequence comprising a signal protein and a desired protein operably linked by an internal ribosome entry site (IRES), and culturing the host cell under suitable conditions so that the signal protein and the desired protein is produced, where the presence of signal protein indicates the presence of desired protein. Regulatory elements and vectors of the invention are useful for the expression of proteins of interest in a host cell. They are useful for producing an immunoglobulin (Ig), preferably secretory Ig. They are useful in the expression of one or more proteins such as erythropoietin, growth hormone, insulin, immunoglobulins, protein C, cytokines and their receptors, hormones, Von Willebrand's factor, lung surfactant, serum albumins, DNase, vascular endothelial growth factor, receptors for hormones or growth factors, rheumatoid factors, nerve growth factors, CD proteins, osteoinductive factors, immunotoxins, bone morphogenetic protein, interferons, colony stimulating factors, interleukins, superoxide dismutase, T-cell receptors, surface membrane proteins, viral antigens, transport proteins, addressins, regulatory proteins, antibodies, chimeric proteins and their fragments. The vectors are particularly useful for expressing G protein coupled receptors and other transmembrane proteins. The retroviral vectors are useful for expressing proteins in mammalian tissue culture host cells, including rat fibroblast cells, bovine kidney cells and human kidney cells. The present sequence is alpha lactalbumin (LA) YP vector used in the invention. The vector comprises the following elements: 5' bovine/human alpha-lactalbumin hybrid promoter, double mutated pre-mRNA processing enhancer (PPE) sequence; bovine alpha-lactalbumin signal peptide, bovine alpha-LA signal peptide, Yersenia pestis antibody heavy chain Fab coding region, encephalomyocarditis virus (ECMV) IRES/bovine alpha-LA signal peptide, Yersenia pestis antibody light chain Fab coding region, woodchuck mRNA processing enhancer (WPRE) sequence and 3' moloney murine leukemia virus (MoMuLV) LTR. (Updated on 07-AUG-2003 to correct OS field.)

Sequence 5691 BP; 1384 A; 1443 C; 1435 G; 1429 T; 0 U; 0 Other;

Query Match 88.9%; Score 56; DB 6; Length 5691;
Best Local Similarity 100.0%; Pred. No. 1-2e-09;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCTTTCATGCCACCCAGGC 56

Db 2403 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCTTTCATGCCACCCAGGC 2458

RESULT 10

AAD28274
ID AAD28274 standard; DNA; 5691 BP.

AC AAD28274;

XX 07-AUG-2003 (revised)

DT 22-APR-2002 (first entry)

XX Alpha-lactalbumin (LA) YP vector.

XX Bovine; alpha-lactalbumin; promoter; pharmaceutical; industrial; ECMV;
KW encephalomyocarditis virus; diagnostic; internal ribosome entry site;
KW IRES; screening; moloney murine leukemia virus; MoMuLV; human; WPRE;
KW woodchuck mRNA processing enhancer; pre-mRNA processing enhancer; PPE;
KW chimeric; ds.

XX Encephalomyocarditis virus.

OS Bos sp.

OS Homo sapiens.

OS Moloney murine leukemia virus.

OS Marmota monax.

OS Yersinia pestis.

OS Unidentified.

OS Chimeric.

XX Key Location/Qualifiers

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FT /tag= a
FT /note= "Bovine/human alpha-lactalbumin 5' flanking
FT region"
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FT /note= "Double mutated PPE sequence"
FT 2403. .2459
FT /tag= c
FT /product= "Bovine alpha-lactalbumin signal peptide coding
FT region"
FT 2460. .3137
FT /tag= d
FT /product= "Yersenia pestis heavy chain Fab gene coding
FT region"
FT 3167. .3742
FT /tag= e
FT /note= "EMCV IRES"
FT 3743. .3799
FT /tag= f
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FT region"
FT 3800. .4441
FT /tag= g
FT /product= "Yersenia pestis light chain Fab gene coding
FT region"
FT 4461. .5052
FT /tag= h
FT /note= "WPRE sequence"
FT 5098. .5691
FT /tag= i
FT /note= "MoMuLV 3' LTR"
XX WO200202738-A2.

XX 10-JAN-2002.

XX 29-JUN-2001; 2001WO-US020710.

XX 03-JUL-2000; 2000US-0215925P.

XX (GALA-) GALA DESIGN INC.

XX Bremel RD, Miller LU, Bleck GT, York D;

XX WPI; 2002-154737/20.

XX Host cell for producing a desired protein and for screening compounds
PT useful for pharmaceutical, industrial, diagnostic and other purposes,
PT comprises multiple integrating vectors having an exogenous gene.

XX Example 1; Fig 14; 191pp; English.

XX The invention relates to a host cell comprising a genome having at least
CC two integrated integrating vectors. The integrating vectors comprise at
CC least one exogenous gene operably linked to a promoter. The host cell is
CC useful for producing a desired protein and for comparing protein
CC functions. The host cells comprises a reporter gene which is from gene
CC fluorescent protein, luciferase, beta-galactosidase and beta-lactamase,
CC and the assaying step further comprises detecting a signal from the
CC reporter gene. The desired protein includes proteins for pharmaceutical,
CC industrial, diagnostic and other purposes. The host cells is useful for
CC indirectly detecting the expression of a desired protein, comprising
CC providing the host cell transfected with a vector encoding a
CC polycistronic sequence comprising a signal protein and a desired protein
CC operably linked by an internal ribosome entry site (IRES), and culturing
CC the host cell under suitable conditions so that the signal protein and
CC the desired protein is produced, where the presence of signal protein
CC indicates the presence of desired protein. The present sequence is alpha
CC lactalbumin (LA) YP vector used in the invention. The vector comprises
CC the following elements: 5' bovine/human alpha-lactalbumin hybrid
CC promoter, double mutated pre-mRNA processing enhancer (PPE) sequence;
CC bovine alpha-lactalbumin signal peptide, bovine alpha-LA signal peptide,
CC Yersenia pestis antibody heavy chain Fab coding region,

CC encephalomyocarditis virus (ECMV) IRES; bovine alpha-LA signal peptide
CC Yersenia pestis antibody light chain Fab coding region, woodchuck mRNA
CC processing enhancer (WPRE) sequence and 3' moloney murine leukemia virus
CC (MoMuLV) LTR. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 5691 BP; 1384 A; 1443 C; 1435 G; 1429 T; 0 U; 0 Other;

Query Match 88.9%; Score 56; DB 6; Length 5691;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCCACCCAGGC 56
Db 2403 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCCACCCAGGC 2458

RESULT 11
ADM68974
ID ADM68974 standard; DNA; 5691 BP.

XX
AC ADM68974;

XX
DT 03-JUN-2004 (first entry)

XX
DE Alpha-lactalbumin (alpha-LA) YP vector DNA.

XX
KW Pharmaceutical; industry; diagnosis; alpha-lactalbumin; alpha-LA; ds; YP.
XX
OS Synthetic.

XX
PN US2003224415-A1.

XX
PD 04-DEC-2003.

XX
PF 26-MAR-2003; 2003US-00397079.

XX
PR 29-JUN-2001; 2001US-00897511.

XX
PR 28-MAR-2002; 2002US-0386357P.

XX
PA (GALA-) GALA DESIGN INC.

XX
PI Bremel RD, Bleck GT, York D, Eakle K;

XX
WPI; 2004-033957/03.

XX
PT Host cell useful for producing proteins for pharmaceuticals, industrial
PT purposes, comprising genome having at least one integrated vector having
PT at least one exogenous gene and lacking selectable marker.

PS
XX Example 1; SEQ ID NO 11; 78pp; English.

XX
XX The invention relates to a host cell comprising a genome comprising at
XX least one integrated integrating vector, where the integrating vector
XX comprises at least one exogenous gene operably linked to a promoter, and
XX where the integrating vector lacks a gene encoding a selectable marker.
XX The invention also relates to a method of transfecting host cells,
XX involving providing a number of host cells comprising a genome and a
XX number of integrating vectors, where the integrating vectors comprise at
XX least one exogenous gene, and where the integrating vectors lack a gene
XX encoding a selectable marker, contacting the host cell with a number of
XX integrating vectors to generate transfected host cells comprising at
XX least one integrated copy of the integrating vector and selecting the
XX transfected host cells. The host cell is useful for producing a protein
XX of interest which involves providing a host cell, where the exogenous
XX gene encodes a protein of interest and culturing the host cell under
XX conditions such that the protein of interest is produced. The integrated
XX exogenous gene is stable in the absence of selection. The integrating
XX vector further comprises a secretion signal sequence operably linked to
XX the exogenous gene. The host cell is useful for the production of
XX proteins for pharmaceuticals and industrial, diagnostic and other
XX purposes, and in the production of multiple variants of proteins,
XX followed by analysis of the activity of the protein variants. This
XX sequence represents alpha-lactalbumin (alpha-LA) YP vector DNA, used in

CC the scope of the invention.

XX
SQ Sequence 5691 BP; 1384 A; 1443 C; 1435 G; 1429 T; 0 U; 0 Other;

Query Match 88.9%; Score 56; DB 12; Length 5691;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCCACCCAGGC 56
Db 2403 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCCACCCAGGC 2458

RESULT 12

ABX35125
ID ABX35125 standard; cDNA; 284 BP.

XX
AC ABX35125;

XX
DT 20-FEB-2003 (first entry)

XX
DE Bovine EST associated with lactation/muscle/fat deposition #290.

XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.

XX
OS Bos Taurus.

XX
PN US2002137139-A1.

XX
PD 26-SEP-2002.

XX
PF 24-SEP-2001; 2001US-00960352.

XX
PR 12-JAN-1999; 99US-0115707P.

XX
PR 11-JAN-2000; 2000US-00480902.

XX
PA (BYAT/) BYATT J C.

XX
PA (MATH/) MATHIALAGAN N.

XX
PA (TAON/) TAO N.

XX
PA (WARR/) WARREN W C.

XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX
WPI; 2003-110599/10.

XX
PT New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.

PS
XX Claim 2; SEQ ID NO 290; 245pp; English.

XX
XX The invention relates to a purified nucleic acid molecule associated with
XX lactation or muscle and fat deposition (designated LMFD), derived from
XX cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX nucleic acid molecule comprising any of 1512 nucleotide sequences,
XX appearing as ABX34836-ABX4947, or complements of them. Also included are
XX ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX acid linked to a promoter and a 3' non-translated sequence that
XX functions in the cell to cause termination of transcription and addition
XX of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX (2) determining a level or pattern of a molecule in a bovine cell or
XX tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX of the 1512 nucleic acid sequences or its complement or fragment) with a
XX complementary nucleic acid molecule obtained from the bovine cell or
XX tissue, where hybridisation between the marker nucleic acid and the
XX complementary nucleic acid permits the detection of the molecule; and (b)
XX detecting the level or pattern of the complementary nucleic acid, where
XX the detection of the complementary nucleic acid is predictive of the
XX level or pattern of the molecule. The LMFD nucleic acid is used for
XX determining a level or pattern of a molecule in a bovine cell or tissue.
XX It is useful for genome mapping, gene identification and analysis, cattle

CC least one integrated copy of the integrating vector and selecting the
CC transfected host cells. The host cell is useful for producing a protein
CC of interest which involves providing a host cell, where the exogenous
CC gene encodes a protein of interest and culturing the host cell under
CC conditions such that the protein of interest is produced. The integrated
CC exogenous gene is stable in the absence of selection. The integrating
CC vector further comprises a secretion signal sequence operably linked to
CC the exogenous gene. The host cell is useful for the production of
CC proteins for pharmaceuticals and industrial, diagnostic and other
CC purposes, and in the production of multiple variants of proteins,
CC followed by analysis of the activity of the protein variants. This
CC sequence represents CMV MN14 vector DNA, used in the scope of the
CC invention.

XX
SQ Sequence 4207 BP; 1030 A; 1202 C; 1058 G; 917 T; 0 U; 0 Other;
Query Match 82.2%; Score 51.8; DB 12; Length 4207;
Best Local Similarity 88.9%; Pred. No. 3.4e-08;
Matches 56; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ATGATGTCCTTTGTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTGTT 60
Db 2847 ATGGCCTCCTTTGTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTGTT 60

Qy 61 AAC 63
Db 2907 ATC 2909

Search completed: October 1, 2005, 13:37:30
Job time : 373.982 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 13:13:06 ; Search time 2924.2 Seconds
(without alignments)
820.069 Million cell updates/sec

Title: US-10-820-777-1

Perfect score: 63

Sequence: 1 atgatgtcctttgtctctct.....atgcaccaccaggtgttaac 63

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	92.1	140	2	BE483233
2	58	92.1	145	2	BE479481
3	58	92.1	149	2	BE487063
4	58	92.1	161	2	BE589418
5	58	92.1	209	2	BF230700
6	58	92.1	321	4	BG687704
7	58	92.1	326	4	BG693760
8	58	92.1	329	2	BE482526
9	58	92.1	330	2	BF230601
10	58	92.1	340	4	BG693834
11	58	92.1	343	2	BE477471
12	58	92.1	375	2	BE485596
13	58	92.1	386	2	BF230784
14	58	92.1	389	4	BG689381
15	58	92.1	395	4	BG690404
16	58	92.1	403	2	BE477823
17	58	92.1	413	2	BF230628
18	58	92.1	417	2	BE485405
19	58	92.1	425	4	BG687739
20	58	92.1	460	2	BE484668
21	58	92.1	464	2	BE588964
22	58	92.1	479	2	BE589398
23	58	92.1	483	2	BE482872
24	58	92.1	490	4	BG690289

25	58	92.1	495	4	BG690292	BA
26	58	92.1	498	2	BE485759	BA
27	58	92.1	509	2	BE478560	BA
28	58	92.1	519	2	BE476701	BA
29	58	92.1	519	2	BE477066	BA
30	58	92.1	524	4	BG693240	BA
31	58	92.1	532	2	BE588671	BA
32	58	92.1	561	4	BG689677	BA
33	58	92.1	581	4	BG691002	BA
34	58	92.1	594	2	BE846304	BA
35	58	92.1	598	2	BE588487	BA
36	58	92.1	612	6	CA034915	B
37	58	92.1	615	4	BG693331	BA
38	58	92.1	618	4	BG692696	BA
39	58	92.1	637	4	BG692107	BA
40	58	92.1	650	2	BF230885	BA
41	58	92.1	651	4	BG690945	BA
42	58	92.1	651	4	BG691660	BA
43	58	92.1	701	7	CK849125	BA
c	56.4	89.5	167	5	BM878960	BA
44	56.4	89.5	214	2	BF230828	BA
45	56.4	89.5	214	2	BF230828	BA

ALIGNMENTS

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LOCUS BE483233 140 bp mRNA linear EST 27-MAR-2003
DEFINITION 169315 BARC SBOV Bos taurus cdna 5', mRNA sequence.
ACCESSION BE483233
VERSION BE483233.1 GI:9602766
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 140)
AUTHORS Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
TITLE Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
JOURNAL Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE 22135956
PubMed 12140684
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tadse@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 13 row: I column: 19
Seq primer: ATTAGGTGACACTATAG.

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/tissue_type="pooled"
/lab_host="DH10B"
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/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

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Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCGCCACCCAGGCTG 58
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Db 18 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCGCCACCCAGGCTG 75

RESULT 2
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LOCUS BE479481 145 bp mRNA linear EST 27-MAR-2003
DEFINITION 184191 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE479481
VERSION BE479481.1 GI:9599014
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 145)
Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
PUBMED 12140684
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGAGTCACGACG
Plate: 139 row: D column: 7
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
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Library made from pooled mRNA isolated from mammary
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states."
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source
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Best Local Similarity 100.0%; Pred. No. 4.5e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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LOCUS BE487063 149 bp mRNA linear EST 27-MAR-2003
DEFINITION 175619 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

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ACCESSION BE487063
VERSION BE487063.1 GI:9606596
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 149)
Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
Analysis of bovine mammary gland EST and functional annotation of
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22135956
PUBMED 12140684
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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Seq primer: ATTTAGTGACACTATAG.
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/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
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Query Match          92.1%; Score 58; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 4.5e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCGCCACCCAGGCTG 58
|||||
Db 15 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGCATCCTATTCCATGCGCCACCCAGGCTG 72

RESULT 4
BE589418
LOCUS BE589418 161 bp mRNA linear EST 27-MAR-2003
DEFINITION 195566 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE589418
VERSION BE589418.1 GI:9842457
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 161)
Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)

```

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MEDLINE
PUBMED
COMMENT
22135956
12140684
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 120 row: L column: 23
Seq primer: ATTTAGTGACACTATAG.
FEATURES
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Location/Qualifiers
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Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
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Best Local Similarity 100.0%; Pred. No. 4.5e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 4 ATGATGTCCTTTGCTCTCTGCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 61
|||||

RESULT 5
BF230700 209 bp mRNA linear EST 27-MAR-2003
LOCUS
DEFINITION
252526 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION
BF230700
VERSION
BF230700.1 GI:11168946
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 209)
Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
12140684
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
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tissues at eight physiological, developmental, and disease
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RESULT 6
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LOCUS
DEFINITION
334904 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION
BG687704
VERSION
BG687704.1 GI:13929505
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 321)
Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
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22135956
12140684
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
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RESULT 7
BG693760
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DEFINITION
ACCESSION  BG693760
VERSION     BG693760.1 GI:13935580
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE  1 (bases 1 to 326)
AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
            Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
            and Quackenbush,J.
TITLE     Analysis of bovine mammary gland EST and functional annotation of
            the Bos taurus gene index
JOURNAL   Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE   22135956
PUBMED    12140684
COMMENT    Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
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                tissues at eight physiological, developmental, and disease
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Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTGCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 58
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Db 12 ATGATGTCCTTTGCTCTCTGCTGCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 69

RESULT 8
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LOCUS      168350 BARC 5BOV Bos taurus cDNA 5', mRNA sequence. EST 27-MAR-2003
DEFINITION
ACCESSION  BE482526
VERSION     BE482526.1 GI:9602059
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE  1 (bases 1 to 330)
AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
            Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
            and Quackenbush,J.
TITLE     Analysis of bovine mammary gland EST and functional annotation of
            the Bos taurus gene index
JOURNAL   Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE   22135956
PUBMED    12140684
COMMENT    Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCGAGTCACGACG
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                tissues at eight physiological, developmental, and disease
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Query Match      92.1%; Score 58; DB 4; Length 326;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9
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LOCUS      252368 BARC 5BOV Bos taurus cDNA 5', mRNA sequence. EST 27-MAR-2003
DEFINITION
ACCESSION  BF230601
VERSION     BF230601.1 GI:11168743
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE  1 (bases 1 to 330)
AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
            Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
            and Quackenbush,J.
TITLE     Analysis of bovine mammary gland EST and functional annotation of
            the Bos taurus gene index
JOURNAL   Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE   22135956
PUBMED    12140684
COMMENT    Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
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Plate: 47 row: N column: 7
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Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS      252368 BARC 5BOV Bos taurus cDNA 5', mRNA sequence. EST 27-MAR-2003
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ACCESSION  BF230601
VERSION     BF230601.1 GI:11168743
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
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            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE  1 (bases 1 to 330)
AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
            Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
            and Quackenbush,J.
TITLE     Analysis of bovine mammary gland EST and functional annotation of
            the Bos taurus gene index
JOURNAL   Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE   22135956
PUBMED    12140684
COMMENT    Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
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Plate: 47 row: N column: 7
Seq primer: ATTTAGTGACACTATAG.
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Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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COMMENT

Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

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 Plate: 109 row: D column: 5
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers

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 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
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ORIGIN

Query Match 92.1%; Score 58; DB 2; Length 330;
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 ACCESSION
 VERSION BG693834.1 GI:13935654
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 ORGANISM Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

1 (bases 1 to 340)
 Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
 Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
 and Quackenbush, J.

Analysis of bovine mammary gland EST and functional annotation of
 the Bos taurus gene index
 Mamm. Genome 13 (7), 373-379 (2002)
 22135956
 12140684

COMMENT

Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414

Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCAGTCACGACG
 Plate: 47 row: O column: 15
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers

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 Library made from pooled mRNA isolated from mammary
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ORIGIN

Query Match 92.1%; Score 58; DB 4; Length 340;
 Best Local Similarity 100.0%; Pred. No. 5.1e-09;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGTCCTCTCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 58
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 LOCUS
 DEFINITION BE477471 161184 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION
 VERSION BE477471.1 GI:9597004
 KEYWORDS
 SOURCE EST.
 ORGANISM Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

1 (bases 1 to 343)
 Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
 Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
 and Quackenbush, J.

Analysis of bovine mammary gland EST and functional annotation of
 the Bos taurus gene index
 Mamm. Genome 13 (7), 373-379 (2002)
 22135956
 12140684

COMMENT

Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414

Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
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PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
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 Location/Qualifiers

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 Library made from pooled mRNA isolated from mammary
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 Best Local Similarity 100.0%; Pred. No. 5.1e-09;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 13:15:56 ; Search time 111.504 Seconds
(without alignments)
924.496 Million cell updates/sec

Title: US-10-820-777-1

Perfect score: 63

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	58	92.1	2044	2	US-08-621-100-3
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4	41.6	66.0	2119	2	US-08-381-691-17
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6	26.6	42.2	8050	4	US-09-949-016-12
7	26	41.3	593	3	US-08-961-083-107
8	26	41.3	593	4	US-09-536-784-107
9	26	41.3	876	2	US-08-928-284-1
10	26	41.3	1506	4	US-05-583-110-1642
11	26	41.3	1515	4	US-09-107-433-2390
12	26	41.3	9711	3	US-08-961-527-167
13	24.8	39.4	601	4	US-09-949-016-69680
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15	24.8	39.4	28136	4	US-09-949-016-16317
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22	24.6	39.0	194937	4	US-09-949-016-17033
23	24.4	38.7	601	4	US-09-949-016-17806
24	24.4	38.7	601	4	US-09-949-016-69682
25	24.4	38.7	601	4	US-09-949-016-109563
26	24.4	38.7	36028	4	US-09-949-016-14761
27	24.2	38.4	6333	4	US-09-949-016-15447

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Sequence 17162, A
Sequence 14837, A
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Sequence 9488, Ap
Sequence 1080, Ap
Sequence 14853, A
Sequence 12705, A
Sequence 17550, A
Sequence 186, App
Sequence 150, App
Sequence 14554, A

ALIGNMENTS

RESULT 1
US-08-071-601-3
; Sequence 3, Application US/08071601
; Patent No. 5530177
; GENERAL INFORMATION:
; APPLICANT: BLECK, GREGORY T.
; APPLICANT: BREMEL, ROBERT D.
; TITLE OF INVENTION: DNA SEQUENCE ENCODING BOVINE
; TITLE OF INVENTION: ALPHA-LACTALBUMIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL
; STREET: 100 E. WISCONSIN AVE., SUITE 1100
; CITY: MILWAUKEE
; STATE: WI
; COUNTRY: USA
; ZIP: 53202-4178
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/071,601
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/744,765
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: F. 3262-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 255-2022
; TELEFAX: (608) 255-2182
; TELEX: 26832 ANDSTARK
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2044 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: signal peptide coding region
; LOCATION: 1943..2043
; FEATURE:
; NAME/KEY: inherited control region for a-lactalbumin
; LOCATION: 1966


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; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/536,784
;   FILING DATE: 30-Oct-1997
;   CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/961,083
;   FILING DATE: OCT-30-1997
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Michelle S. Marks
;   REGISTRATION NUMBER: 41,971
;   REFERENCE/DOCKET NUMBER: PB340P3
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (301) 309-8504
;   TELEFAX: (301) 309-8512
;
; INFORMATION FOR SEQ ID NO: 107:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 593 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
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; RESULT 9
; US-09-536-284-1/c
; Sequence 1, Application US/08928284
; Patent No. 5882871
; GENERAL INFORMATION:
;   APPLICANT: Burnham, Martin K.
;   TITLE OF INVENTION: No. 5882871el Saliva Binding Prot
;   TITLE OF INVENTION: ein
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Dechert, Price & Rhoads
;     STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
;     CITY: Philadelphia
;     STATE: PA
;     COUNTRY: USA
;     ZIP: 19103-2793
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSeq for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/928,284
;     FILING DATE:
;   CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 60/026,682
;       FILING DATE: 24-SEP-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Dickinson, Q. Todd
;       REGISTRATION NUMBER: 28,354
;       REFERENCE/DOCKET NUMBER: P50543
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 215/994-2252
;       TELEFAX: 215/994-2222
;       TELEX:
;   INFORMATION FOR SEQ ID NO: 1:
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; US-09-583-110-1642/c
; Sequence 1642, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
;   APPLICANT: Lynn Doucette-Stamm et al.
;   TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;   TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
;   FILE REFERENCE: PATH00-07A
;   CURRENT APPLICATION NUMBER: US/09/583,110
;   CURRENT FILING DATE: 2000-05-26
;   PRIOR APPLICATION NUMBER: US 09/107,433
;   PRIOR FILING DATE: 1998-06-30
;   PRIOR APPLICATION NUMBER: US 60/085,131
;   PRIOR FILING DATE: 1998-05-12
;   PRIOR APPLICATION NUMBER: US 60/051,553
;   PRIOR FILING DATE: 1997-07-02
;   NUMBER OF SEQ ID NOS: 5322
;   SEQ ID NO 1642
;   LENGTH: 1506
;   TYPE: DNA
;   ORGANISM: Streptococcus pneumoniae
;
; US-09-583-110-1642
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; Best Local Similarity 70.0%; Pred. No. 9;
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; RESULT 11
; US-09-107-433-2390/c
; Sequence 2390, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
;   APPLICANT: Lynn A Doucette-Stamm and David Bush
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
;   TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
;   TITLE OF INVENTION: THERAPEUTICS
;   NUMBER OF SEQUENCES: 5206
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;     STREET: 100 Beaver Street
;     CITY: Waltham
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02354
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: CD/ROM ISO9660
;     COMPUTER: <Unknown>
;     OPERATING SYSTEM: <Unknown>
;     SOFTWARE: <Unknown>
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/107,433
;     FILING DATE: 30-Jun-1998
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; ORGANISM: Human

US-09-949-016-69681

Query Match 39.4%; Score 24.8; DB 4; Length 601;
Best Local Similarity 67.3%; Pred. No. 19;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 5 TGTCTTTGTCTCTCTGCTGCTAGGCATCCTATTCCATGCCACCCAGGC 56
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Db 128 TGCCAGTGTTCACCTGCTCCTGAGTCCTTCTTATGCTTGGCACCAGGC 77

RESULT 15

US-09-949-016-16317/C
; Sequence 16317, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16317
; LENGTH: 28136
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(28136)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-16317

Query Match 39.4%; Score 24.8; DB 4; Length 28136;
Best Local Similarity 67.3%; Pred. No. 55;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 7 TCCTTTCTCTCTGCTCCTGCTAGGCATCCTATTCCATGCCACCCAGGCTG 58
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Db 13562 TCCTTTATCTCTCTTTTTTTTGAGACAGAGTTTGTCTGTCACCCAGGCTG 13511

Search completed: October 1, 2005, 15:41:11
Job time : 113.504 secs

Db 3658 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 3715
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RESULT 2
US-10-401-000-4
; Sequence 4, Application US/10401000
; Publication No. US20040038304A1
; GENERAL INFORMATION:
; APPLICANT: Bremel, Robert D.
; APPLICANT: Eakle, Kurt
; APPLICANT: Imboden, Michael
; TITLE OF INVENTION: Antibody Libraries
; FILE REFERENCE: GALA-07886
; CURRENT APPLICATION NUMBER: US/10/401,000
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 60/368,808
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/371,299
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 7472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-401-000-4

Query Match 89.8%; Score 56.6; DB 18; Length 7472;
Best Local Similarity 93.7%; Pred. No. 6.1e-11;
Matches 59; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTGTT 60
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Db 3727 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 3786
61 AAC 63
3787 ATC 3789

RESULT 3
US-10-401-000-3
; Sequence 3, Application US/10401000
; Publication No. US20040038304A1
; GENERAL INFORMATION:
; APPLICANT: Bremel, Robert D.
; APPLICANT: Eakle, Kurt
; APPLICANT: Imboden, Michael
; TITLE OF INVENTION: Antibody Libraries
; FILE REFERENCE: GALA-07886
; CURRENT APPLICATION NUMBER: US/10/401,000
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 60/368,808
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/371,299
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 7490
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-401-000-3

Query Match 89.8%; Score 56.6; DB 18; Length 7490;
Best Local Similarity 93.7%; Pred. No. 6.1e-11;
Matches 59; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTGTT 60
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Db 3727 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 3786
61 AAC 63
3787 ATC 3789

RESULT 4
US-09-930-377B-1
; Sequence 1, Application US/09930377B
; Patent No. US20020144296A1
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Matthew B.
; APPLICANT: Donovan, Sharon M.
; APPLICANT: Bleck, Gregory T.
; APPLICANT: Monaco-Seigel, Marcia
; TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
; FILE REFERENCE: 66-00
; CURRENT APPLICATION NUMBER: US/09/930,377B
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,474
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4532
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alpha-LA/IGF-I
; OTHER INFORMATION: gene construct
US-09-930-377B-1

Query Match 89.5%; Score 56.4; DB 9; Length 4532;
Best Local Similarity 98.3%; Pred. No. 6.8e-11;
Matches 57; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 58
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Db 1989 ATGATGTCCTTTGCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 2046

RESULT 5
US-10-676-566-1
; Sequence 1, Application US/10676566
; Publication No. US20040064841A1
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Matthew B.
; APPLICANT: Donovan, Sharon M.
; APPLICANT: Bleck, Gregory T.
; APPLICANT: Monaco-Seigel, Marcia
; TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
; FILE REFERENCE: 66-00A
; CURRENT APPLICATION NUMBER: US/10/676,566
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/225,474
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4532
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alpha-LA/IGF-I
; OTHER INFORMATION: gene construct
US-10-676-566-1

Query Match 89.5%; Score 56.4; DB 18; Length 4532;
Best Local Similarity 98.3%; Pred. No. 6.8e-11;
Matches 57; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ATGATGTCCTTTGCTCTCTGCTCTCTGCTAGGCATCCTATTCCATGCAACCCAGGCTG 58
Db 1989 ATGATGTCCTTTGCTCTCTGCTCTCTGCTAGGAATCCTATTCCATGCAACCCAGGCTG 2046

RESULT 6
US-09-897-006-11
; Publication No. US20020106729A1
; Sequence 11, Application US/09897006
; Patent No. US20020106729A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Expression Vectors
; FILE REFERENCE: GALA-06415
; CURRENT APPLICATION NUMBER: US/09/897,006
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,851
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-006-11

Query Match 88.9%; Score 56; DB 9; Length 5691;
Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTCTGCTAGGCATCCTATTCCATGCAACCCAGG 56
Db 2403 ATGATGTCCTTTGCTCTCTGCTCTCTGCTAGGCATCCTATTCCATGCAACCCAGG 2458

RESULT 7
US-09-897-511A-11
; Publication No. US20030092882A1
; Sequence 11, Application US/09897511A
; Patent No. US20030092882A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory
; APPLICANT: Bleck, Robert
; APPLICANT: Miller, Linda
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/09/897,511A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-511A-11

Query Match 88.9%; Score 56; DB 10; Length 5691;
Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTCTGCTAGGCATCCTATTCCATGCAACCCAGG 56
Db 2403 ATGATGTCCTTTGCTCTCTGCTCTCTGCTAGGCATCCTATTCCATGCAACCCAGG 2458

RESULT 8
US-10-397-079-11
; Publication No. US10397079
; Sequence 11, Application US/10397079
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; Publication No. US20030224415A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Robert
; APPLICANT: Miller, Linda
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/10/397,079
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/897,511A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-397-079-11

Query Match 88.9%; Score 56; DB 17; Length 5691;
Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTCTGCTAGGCATCCTATTCCATGCAACCCAGG 56
Db 2403 ATGATGTCCTTTGCTCTCTGCTCTCTGCTAGGCATCCTATTCCATGCAACCCAGG 2458

RESULT 9
US-10-759-315-11
; Publication No. US20040235173A1
; Sequence 11, Application US/10759315
; Patent No. US20040235173A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory T.
; APPLICANT: Bleck, Robert D.
; APPLICANT: Miller, Linda U.
; TITLE OF INVENTION: Production of Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-08484
; CURRENT APPLICATION NUMBER: US/10/759,315
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 5691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-759-315-11

Query Match 88.9%; Score 56; DB 20; Length 5691;
Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCTCTGCTAGGCATCCTATTCCATGCAACCCAGG 56
Db 2403 ATGATGTCCTTTGCTCTCTGCTCTCTGCTAGGCATCCTATTCCATGCAACCCAGG 2458

RESULT 10
US-10-947-881-11
; Publication No. US20050060762A1
; Sequence 11, Application US/10947881
; Patent No. US20050060762A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Expression Vectors
; FILE REFERENCE: GALA-06415
; CURRENT APPLICATION NUMBER: US/10/947,881
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; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US/09/897,006
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,851
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-947-881-11

Query Match      88.9%; Score 56; DB 21; Length 5691;
Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGTCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGC 56
Db 2403 ATGATGTCCTTTGTCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGC 2458

RESULT 11
US-11-018-895-11
; Sequence 11, Application US/11018895
; Publication No. US20050100952A1
; GENERAL INFORMATION:
; APPLICANT: Bremel, Robert
; APPLICANT: Miller, Linda
; APPLICANT: Bremel, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/11/018,895
; CURRENT FILING DATE: 2004-12-21
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-018-895-11

Query Match      88.9%; Score 56; DB 23; Length 5691;
Best Local Similarity 100.0%; Pred. No. 9.9e-11;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGTCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGC 56
Db 2403 ATGATGTCCTTTGTCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGC 2458

RESULT 12
US-09-960-352-290
; Sequence 290, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
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; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 290
; LENGTH: 284
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 02-LIB2809-016-Q1-E1-A5
US-09-960-352-290

Query Match      87.3%; Score 55; DB 9; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ATGTCCTTTGTCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 58
Db 106 ATGTCCTTTGTCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTG 160

RESULT 13
US-09-897-006-4
; Sequence 4, Application US/09897006
; Patent No. US20020106729A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Expression Vectors
; FILE REFERENCE: GALA-06415
; CURRENT APPLICATION NUMBER: US/09/897,006
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,851
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 4207
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-006-4

Query Match      82.2%; Score 51.8; DB 9; Length 4207;
Best Local Similarity 88.9%; Pred. No. 3.5e-09;
Matches 56; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 2847 ATGCGCTCTCTTTGTCTCTCTGCTCTGCTAGGATCCTATTCCATGCCACCCAGGCTGT 60

Qy 61 AAC 63
Db 2907 ATC 2909

RESULT 14
US-09-897-511A-4
; Sequence 4, Application US/09897511A
; Publication No. US20030092882A1
; GENERAL INFORMATION:
; APPLICANT: Bremel, Robert
; APPLICANT: Miller, Linda
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/09/897,511A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 4207
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetic
US-09-897-511A-4
Query Match      82.2%; Score 51.8; DB 10; Length 4207;
Best Local Similarity 88.9%; Pred. No. 3.5e-09;
Matches 56; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTGTT 60
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Qy 61 AAC 63
Db 2907 ATC 2909
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RESULT 15
US-10-397-079-4
; Sequence 4, Application US/10397079
; Publication No. US20030224415A1
; GENERAL INFORMATION:
; APPLICANT: Bremel, Robert
; APPLICANT: Miller, Linda
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/10/397,079
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/897,511A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 4207
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-397-079-4
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Query Match      82.2%; Score 51.8; DB 17; Length 4207;
Best Local Similarity 88.9%; Pred. No. 3.5e-09;
Matches 56; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGATGTCCTTTGCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCTGTT 60
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Qy 61 AAC 63
Db 2907 ATC 2909
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Search completed: October 1, 2005, 15:58:56
Job time : 588.628 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 12:21:16 ; Search time 858.407 Seconds
(without alignments)
2822.391 Million cell updates/sec

Title: US-10-820-777-2

Perfect score: 50

Sequence: 1 atgaactctctcattcttac.....gctgttgctgccaggttaac 50

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	39	78.0	1071	ABAJ5430	AY005430 Bubalus b
3	39	78.0	1123	BOVCASA	M31123 Bovine alph
4	39	78.0	1123	AR266832	AR266832 Sequence
5	39	78.0	1134	BOVCASAS1	M38641 Bovine alph
6	39	78.0	1172	BTCASBS1	X00564 Bovine mRNA
7	39	78.0	1554	CHASICAS	X72221 C.hircus mr
8	39	78.0	19406	CHI504712	AY504712 Capra hir
9	39	78.0	19408	CHI504710	AY504710 Capra hir
10	39	78.0	19414	CHI504711	AY504711 Capra hir
11	39	78.0	22069	BTAS1C	X59856 B.taurus ge
12	39	78.0	195534	AC134173	AC134173 Bos tauru
13	38	76.0	1110	OACASAS1R	X03237 Sheep mRNA
14	37.4	74.8	1126	CHASICAR	X59836 C.hircus mr
15	35.8	71.6	51	AR002676	AR002676 Sequence
16	35.8	71.6	51	AR118420	AR118420 Sequence
17	35.8	71.6	51	6	I43703 Sequence 37
18	35.8	71.6	1139	AY040862	AY040862 Equus cab
19	34.8	69.6	1094	CDRO12628	AY012628 Camelus d

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21	32.6	65.2	981	9	HSALS1C	X78416 H.sapiens a
22	32.6	65.2	990	6	AR448210	AR448210 Sequence
23	32.6	65.2	161549	2	AC024676	AC024676 Homo sapi
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25	32.6	65.2	179273	9	AC108941	AC108941 Homo sapi
26	32.4	64.8	39	6	AR027325	AR027325 Sequence
27	31.6	63.2	1134	4	SSAS1CASM	X54973 S.scrofa mr
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29	31	62.0	668	6	AX359938	AX359938 Sequence
30	31	62.0	688	6	AX382152	AX382152 Sequence
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32	31	62.0	1379	10	MUSACASB	M36780 Mouse alpha
33	31	62.0	1397	10	BC008278	BC008278 Mus muscu
34	31	62.0	1409	10	BC006024	BC006024 Mus muscu
35	31	62.0	1411	10	BC002101	BC002101 Mus muscu
36	31	62.0	1411	10	BC040246	BC040246 Mus muscu
37	31	62.0	1432	10	BC003859	BC003859 Mus muscu
38	31	62.0	119681	10	AC102017	AC102017 Mus muscu
39	31	62.0	182534	10	AC074046	AC074046 Mus muscu
40	31	62.0	228840	2	AC097835	AC097835 Rattus no
41	30.4	60.8	1000	10	CSCASB	X00938 Guinea-pig
42	30	60.0	588	6	CQ603756	CQ603756 Sequence
43	30	60.0	717	6	AX525513	AX525513 Sequence
44	29.4	58.8	1018	4	AY049939	AY049939 Equus cab
45	29.4	58.8	1130	4	OCCASA	X13042 Rabbit mRNA

ALIGNMENTS

RESULT 1	AY344966	642 bp	mRNA	linear	MAM 01-AUG-2004
LOCUS	AY344966	642 bp	mRNA	linear	MAM 01-AUG-2004
DEFINITION	Capra hircus CSCN1 mRNA, complete cds.				
ACCESSION	AY344966				
VERSION	AY344966.1	GI:37962702			
KEYWORDS	Capra hircus (goat)				
SOURCE	Capra hircus				
ORGANISM	Capra hircus				

REFERENCE	1 (bases 1 to 642)
AUTHORS	Pelignini, M., Parma, P. and Vlacco, S.
TITLE	A new CASAS1 variant protein in goat
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 642)
AUTHORS	Pelignini, M., Parma, P. and Vlacco, S.
TITLE	Direct Submission
JOURNAL	Submitted (17-JUL-2003) LEA- Laboratorio Epigenetica Applicata, Istituto Sperimentale Italiano 'Lazzaro Spallanzani', Via Giovanni XIII 7, Lodi, Lodi 26900, Italy

FEATURES	Location/Qualifiers
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	/mol_type="mRNA"
	/db_xref="taxon:9925"

CDS

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ORIGIN

Query Match 78.0%; Score 39; DB 4; Length 642;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGAACTTCTCATCTTACCTTACCTGCTTGTGGCTGTGCT 39
Db 1 ATGAACTTCTCATCTTACCTTACCTGCTTGTGGCTGTGCT 39

RESULT 2
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LOCUS BBAJ5430 1071 bp mRNA linear MAM 28-OCT-1998
DEFINITION Bubalus bubalis mRNA for ASI-casein.
ACCESSION AJ005430
VERSION AJ005430.1 GI:3776016
KEYWORDS asi-casein.
SOURCE Bubalus bubalis (water buffalo)
ORGANISM Bubalus bubalis
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bubalus.

REFERENCE 1
AUTHORS Das, P., Jain, S. and Garg, L.C.
TITLE cDNA cloning and sequencing of asi-casein in Bubalus bubalis
JOURNAL Unpublished
REFERENCE 2
AUTHORS Das, P.
TITLE Direct Submission
JOURNAL Submitted (05-APR-1998) Das P., National Institute of Immunology,
Gene Regulation Laboratory, Aruna Asaf Ali Marg, New Delhi- 110067,
INDIA
REMARK Revised by [3]
REFERENCE 3
AUTHORS Das, P.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-1998) Das P., National Institute of Immunology,
Gene Regulation Laboratory, Aruna Asaf Ali Marg, New Delhi- 110067,
INDIA
COMMENT On Oct 20, 1998 this sequence version replaced gi:3063736.
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/db_xref="taxon:89462"
/tissue_type="mammary gland"
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polyA_signal 1050. .1055
polyA_site 1067

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Query Match 78.0%; Score 39; DB 4; Length 1071;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCTCATCTTACCTTACCTGCTTGTGGCTGTGCT 39
Db 1 ATGAACTTCTCATCTTACCTTACCTGCTTGTGGCTGTGCT 39

RESULT 3
BOVCASA
LOCUS BOVCASA 1123 bp mRNA linear MAM 26-APR-1993
DEFINITION Bovine alpha-s1-casein mRNA, complete cds.
ACCESSION M33123
VERSION M33123.1 GI:162791
KEYWORDS alpha-s1-casein
SOURCE Bos taurus (cow)

Query Match 78.0%; Score 39; DB 6; Length 1123;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGAACTTCTCATCTTACCTTACCTGCTTGTGGCTGTGCT 102

RESULT 4
AR266832
LOCUS AR266832 1123 bp mRNA linear PAT 10-APR-2003
DEFINITION Sequence 40 from patent US 6495344.
ACCESSION AR266832
VERSION AR266832.1 GI:29696163
KEYWORDS Unknown.
SOURCE Unclassified.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1123)
AUTHORS Carr, N.G. and Mann, N.H.
TITLE Phenylalanine-free protein and DNA coding therefor
JOURNAL Patent: US 6495344-A 40 17-DEC-2002;
FEATURES
source
1. .1123
/mol_type="mRNA"

Query Match 78.0%; Score 39; DB 6; Length 1123;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCTCATCTTACCTTACCTGCTTGTGGCTGTGCT 39
Db 64 ATGAACTTCTCATCTTACCTTACCTGCTTGTGGCTGTGCT 102

RESULT 5
BOVCASA1
LOCUS BOVCASA1 1123 bp mRNA linear MAM 26-APR-1993
DEFINITION Bovine alpha-s1-casein mRNA, complete cds.
ACCESSION M33123
VERSION M33123.1 GI:162791
KEYWORDS alpha-s1-casein
SOURCE Bos taurus (cow)

Query Match 78.0%; Score 39; DB 6; Length 1123;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCTCATCTTACCTTACCTGCTTGTGGCTGTGCT 39
Db 64 ATGAACTTCTCATCTTACCTTACCTGCTTGTGGCTGTGCT 102

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DEFINITION Bovine alpha-S-1 casein mRNA, complete cds.
ACCESSION  M38641
VERSION    M38641.1 GI:162793
KEYWORDS   casein.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
REFERENCE  1 (bases 1 to 1134)
AUTHORS   Gorodetskii,S.I., Zakhar'ev,V.M., Kyarshulite,D.R.,
           Kapelinskaya,T.V. and Skryabin,K.G.
TITLE     Cloning and nucleotide sequence of cDNA for bovine alpha-S1-casein
JOURNAL   Biochimia 51, 1402-1409 (1986)
COMMENT   Original source text: Bovine mammary gland, cDNA to mRNA.
FEATURES   source
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            /db_xref="taxon:9913"
            /tissue_type="mammary gland"
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            /db_xref="GI:162794"
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ORIGIN
Query Match      78.0%; Score 39; DB 4; Length 1134;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 64 ATGAAACTTCATCCTTACCTGCTGTGTGGCTGTGCT 102
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RESULT 6
BTCASBS1
LOCUS      Bovine mRNA for pre-alpha S1-casein B.
DEFINITION
ACCESSION  X00564
VERSION    X00564.1 GI:175
KEYWORDS   alpha S1-casein; casein B.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
           Bovinae; Bos.
REFERENCE  1 (bases 1 to 1172)
AUTHORS   Stewart,A.F., Willis,I.M. and Mackinlay,A.G.
TITLE     Nucleotide sequences of bovine alpha S1- and kappa-casein cDNAs
JOURNAL   Nucleic Acids Res. 12 (9), 3895-3907 (1984)
MEDLINE   84221403
PUBMED    6328443
REFERENCE  2 (bases 1 to 1172)
AUTHORS   Stewart,A.
TITLE     Direct Submission
JOURNAL   Submitted (19-AUG-1986)
COMMENT   Data kindly reviewed (19-AUG-1986) by A. Stewart.
FEATURES   Location/Qualifiers
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               ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCATCCTTACCTGCTGTGTGGCTGTGCT 39
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Db 101 ATGAAACTTCATCCTTACCTGCTGTGTGGCTGTGCT 139
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RESULT 7
CHASICAS
LOCUS      C.hircus mRNA for alpha S1 Casein E allele.
DEFINITION
ACCESSION  X72221
VERSION    X72221.1 GI:311942
KEYWORDS   alpha-s1-casein; LINE element.
SOURCE     Capra hircus (goat)
ORGANISM   Capra hircus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
           Caprinae; Capra.
REFERENCE  1
AUTHORS   Perez,M.J., Leroux,C., Bonastre,A.S. and Martin,P.
TITLE     Occurrence of a LINE sequence in the 3' UTR of the goat alpha
           s1-casein E-encoding allele associated with reduced protein
           synthesis level
           Gene 147 (2), 179-187 (1994)
           95011611
           PUBMED    7926797
REFERENCE  2 (bases 1 to 1554)
AUTHORS   Jansa,M.
TITLE     Direct Submission
JOURNAL   Submitted (27-MAY-1993) M. Jansa, Inst National de la Recherche
           Agronomique (INRA), Lab de Genetique Biochimique, INRA-CRJ 78350,
           Jouy-en-Josas, FRANCE
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misc_feature SERVLGVLEQLLKKYNVDPQLSIVPKSAREQLHMKNGPNPAHQKQPMIAVNOELAYF
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complement (1232..1295)
polyA_signal /note="LINE element"
ORIGIN 1535..1540

Query Match 78.0%; Score 39; DB 4; Length 1554;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACCTTCATCCTTACCTGTCTGTGTGGCTGTGCT 39
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Db 28 ATGAACCTTCATCCTTACCTGTCTGTGTGGCTGTGCT 66
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RESULT 8
CHI504712 19406 bp DNA linear MAM 11-JUN-2003
LOCUS Capra hircus csnlS1 gene for alpha s1 casein, allele N, exons 1-19.
DEFINITION AJ504712
ACCESSION AJ504712
VERSION AJ504712.2 GI:31620958
KEYWORDS alpha s1 casein; csnlS1 gene.
SOURCE Capra hircus (goat)
ORGANISM Capra hircus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Capra.

REFERENCE 1
AUTHORS Ramunno, L.
TITLE Molecular characterization of the goat CSN1S1 N allele
JOURNAL Unpublished

REFERENCE 2
AUTHORS Ramunno, L.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2002) Ramunno L., Sc. zootechnica e Ispezione
Alimenti, Universita di Napoli Federico II, via Universita 133,
Portici (Na), Italia, 80055, ITALY
revised by [3]

REFERENCE 3 (bases 1 to 19406)
AUTHORS Ramunno, L.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-2003) Ramunno L., Sc. zootechnica e Ispezione
Alimenti, Universita di Napoli Federico II, via Universita 133,
Portici (Na), Italia, 80055, ITALY
On Jun 12, 2003 this sequence version replaced gi:22796158.

COMMENT FEATURES
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10633..10656,10747..10800,12149..12190,12834..12857,
14052..14093,15000..15026,15972..15995,16791..16945,
17532..17575,18372..18756)
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exon
intron

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10747..10800,12149..12167)
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Best Local Similarity 100.0%; Pred. NO. 0.00031;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3416 ATGAACCTTCATCCTTACCTTGCTTGCTGGCTGTTGCT 3454
RESULT 9
CHI504710
LOCUS 19408 bp DNA linear MAM 21-JUL-2004
DEFINITION Capra hircus csn1S1 gene for alpha s1 casein, allele A, exons 1-19.
ACCESSION AJ504710
VERSION AJ504710.2 GI:31620955
KEYWORDS alpha s1 casein; csn1S1 gene.
SOURCE Capra hircus (goat)
ORGANISM Capra hircus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Capra.
REFERENCE 1
AUTHORS Ramunno L., Cosenza G., Rando A., Illario R., Gallo D., Di
Berardino D. and Masina P.
TITLE The goat alpha s1-casein gene: gene structure and promoter analysis
JOURNAL Gene 334, 105-111 (2004)
PUBMED 15256260
REFERENCE 2
AUTHORS Ramunno L.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2002) Ramunno L., Sc. Zootechniche e Ispezione
Alimenti, Università di Napoli Federico II, via Università, 133,
Portici (Na), Italy, 80055, ITALY
REMARK 3 (bases 1 to 19408)
AUTHORS Ramunno L.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-2003) Ramunno L., Sc. Zootechniche e Ispezione
Alimenti, Università di Napoli Federico II, via Università, 133,
Portici (Na), Italy, 80055, ITALY
COMMENT On Jun 12, 2003 this sequence version replaced gi:22796154.
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10635. .10658,10749. .10802,12151. .12192,12836. .12859,
14054. .14095,15002. .15028,15974. .15997,16793. .16947,
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RESULT 10
LOCUS   CHI504711                      19414 bp    DNA    linear    MAM 27-JUN-2003
DEFINITION   Capra hircus csn1s1 gene for alpha s1 casein, allele F, exons 1-19.
ACCESSION   AJ504711
VERSION     AJ504711.2 GI:31620956
KEYWORDS    alpha s1 casein; csn1s1 gene.
SOURCE      Capra hircus (goat)
ORGANISM    Capra hircus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Caprinae; Capra.

REFERENCE 1
AUTHORS    Ramunno,L.
TITLE      Molecular characterization of the goat CSN1S1 F allele
JOURNAL    Unpublished
REFERENCE 2
AUTHORS    Ramunno,L.
TITLE      Direct Submission
JOURNAL    Submitted (01-AUG-2002) Ramunno L., Sc. Zootechniche e Ispezione
            Alimenti, Universita di Napoli Federico II, via Universita 133,
            Portici (Na), 80055 Italia, ITALY
REMARK     revised by [3]
REFERENCE 3
AUTHORS    Ramunno,L.
TITLE      Direct Submission
JOURNAL    Submitted (02-JUN-2003) Ramunno L., Sc. Zootechniche e Ispezione
            Alimenti, Universita di Napoli Federico II, via Universita 133,
            Portici (Na), 80055 Italia, ITALY
COMMENT    On Jun 12, 2003 this sequence version replaced gi:22796156.
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            /chromosome="6"
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            6552..6575,6999..7022,7611..7634,8328..8351,9866..9897,
            10650..10673,10764..10817,12166..12207,12851..12874,
            14069..14110,15010..15036,15982..16005,16801..16955,
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            10764..10817,12166..12184)
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            mRNA

            5'UTR
            exon
            intron
            exon
            variation
            intron
            CDS

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Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAGTCTCATCCTTACCTGCTTGTGGCTGCTGCT 39
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Db 3415 ATGAAGTCTCATCCTTACCTGCTTGTGGCTGCTGCT 3453
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RESULT 11

BTAS1C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BTAS1C
B.taurus gene for alpha-S1-casein.
X59856
X59856.1 GI:91
alpha-s1-casein; milk protein; phosphoprotein.
Bos taurus (cow)
Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 22069)
Koczan,D., Hobom,G. and Seyfert,H.M.
Genomic organization of the bovine alpha-S1 casein gene
Nucleic Acids Res. 19 (20), 5591-5596 (1991)
92051301
PUBMED
1658736
REFERENCE
2 (bases 1 to 22069)
Koczan,D.
Direct Submission
Submitted (28-MAY-1991) D. Koczan, Inst f Mikro- und,
Molekularbiologie / JLU, Frankfurterstr. 107, 6300 Giessen, FRG
For related sequences see Stewart A.F., NAR 12:3895-3907(1984) and
Yu-Lee L., NAR 14:1883-1902(1986).
FEATURES
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11328. .11351,11442. .11495,13027. .13068,13716. .13739,
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6517. .6555
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Query Match      78.0%; Score 39; DB 4; Length 22069;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCATCCTTACTGCTGTGCTGTGCT 39
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Db 3570 ATGAACTTCATCCTTACTGCTGTGCTGTGCT 3608
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RESULT 12
AC134173
DEFINITION Bos taurus clone RP42-254113, WORKING DRAFT SEQUENCE, 26 unordered
            195534 bp DNA linear HTG 27-SEP-2002
            pieces.
ACCESSION AC134173
VERSION AC134173.1 GI:23306007
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

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REFERENCE AUTHORS

1 (bases 1 to 195534)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Albrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyte,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwono,G., Oraguene,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,O., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Woodson,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 195534)

Worley,K.C.

Direct Submission

Submitted (24-SEP-2002)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 195534)

Worley,K.C.

Direct Submission

Submitted (27-SEP-2002)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine

Center code: BCM

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: VUAE

Center clone name: RP42-254113

Summary Statistics

Sequencing vector: M13;

Chemistry: Dye-primer Bodydy; 82% of reads

Chemistry: Dye-terminator Big Dye; 18% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 185623 bases at least Q40

Consensus quality: 190257 bases at least Q30

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Consensus quality: 192466 bases at least Q20

Estimated insert size: 204493; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently

* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2358: contig of 2358 bp in length
* 2359 2458: gap of unknown length
* 2459 5619: contig of 3161 bp in length
* 5620 5719: gap of unknown length
* 5720 8310: contig of 2591 bp in length
* 8311 8410: gap of unknown length
* 8411 11002: contig of 2592 bp in length
* 11003 14386: contig of 3284 bp in length
* 14387 17148: gap of unknown length
* 17149 17249: contig of 2663 bp in length
* 17250 21414: contig of 4165 bp in length
* 21415 25171: contig of 3657 bp in length
* 25172 30645: contig of 5374 bp in length
* 30646 30745: gap of unknown length
* 30746 36182: contig of 5437 bp in length
* 36183 36282: gap of unknown length
* 36283 41956: contig of 5674 bp in length
* 41957 42056: gap of unknown length
* 42057 48094: contig of 6038 bp in length
* 48095 48194: gap of unknown length
* 48195 53214: contig of 5020 bp in length
* 53215 53314: gap of unknown length
* 53315 58849: contig of 5535 bp in length
* 58850 66144: contig of 7195 bp in length
* 66145 66244: gap of unknown length
* 66245 73034: contig of 6789 bp in length
* 73035 73133: gap of unknown length
* 73134 80030: contig of 6897 bp in length
* 80031 80130: gap of unknown length
* 80131 87761: contig of 7631 bp in length
* 87762 87861: gap of unknown length
* 87862 95726: contig of 7865 bp in length
* 95727 95826: gap of unknown length
* 95827 105054: contig of 9228 bp in length
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* 105155 116716: contig of 11562 bp in length
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* 138141 138240: gap of unknown length
* 138241 150687: contig of 12447 bp in length
* 150688 150787: gap of unknown length
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* 166515 195534: contig of 29020 bp in length.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACCTCTCATCTTACCTGCTCTTGCGCTGTGGCT 39
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RESULT 13

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LOCUS OACSAS1R 1110 bp mRNA linear MAM 23-FEB-1995
DEFINITION Sheep mRNA for alpha-S1-casein.
ACCESSION X03237
VERSION X03237.1 GI:1247
KEYWORDS alpha-S1-casein; casein; secretory protein.
SOURCE Ovis aries (sheep)
ORGANISM Ovis aries

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.

REFERENCE 1 (bases 1 to 1110)

AUTHORS Mercier,J.C., Gaye,P., Soulier,S., Hue-Delahaie,D. and Vilotte,J.L.
TITLE Construction and identification of recombinant plasmids carrying
cDNAs coding for ovine alpha S1-, alpha S2-, beta-, kappa-casein
and beta-lactoglobulin. Nucleotide sequence of alpha S1-casein cDNA

JOURNAL Biochimie 67 (9), 959-971 (1985)

MEDLINE 86104473

PUBMED 3002501

COMMENT Data kindly reviewed (12-SEP-1986) by J-C. Mercier.

FEATURES

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/db_xref="GI:1248"

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mat_peptide 107..679

polyA_signal /product="alpha-S1-casein"

polyA_site 1088..1093

1110

ORIGIN

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Best Local Similarity 97.4%; Pred. No. 0.00081;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 14

CHAS1CAR
LOCUS CHAS1CAR 1126 bp mRNA linear MAM 20-JUL-1992
DEFINITION C.hircus mRNA for as1-casein.
ACCESSION X59836
VERSION X59836.1 GI:953
KEYWORDS as1 gene; casein; milk protein.
SOURCE Capra hircus (goat)

ORGANISM Capra hircus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Capra
1 (bases 1 to 1126)
Leroux, C., Mazure, N. and Martin, P.
Mutations away from splice site recognition sequences might
cis-modulate alternative splicing of goat alpha s1-casein
transcripts. Structural organization of the relevant gene
J. Biol. Chem. 267 (9), 6147-6157 (1992)

JOURNAL 92210588
MEDLINE 1372900
PUBMED 1372900

REFERENCE 2 (bases 1 to 1126)
AUTHORS Martin, P.
TITLE Direct Submission
JOURNAL Submitted (27-MAY-1991) P. Martin, Lab. de Genetique biochimique,
INRA, 78352 Jouy-en-Josas, France

FEATURES
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gene
mRNA
CDS

Query Match 74.8%; Score 37.4; DB 4; Length 1126;
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RESULT 15
AR002676
LOCUS AR002676 51 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 37 from patent US 5741957.
ACCESSION AR002676
VERSION AR002676.1 GI:3964230
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 51)
AUTHORS Deboer, H.A., Strijker, R., Heyneker, H.L., Platenburg, G., Lee, S. He.,
Pieper, F. and Krimpenfort, P.J.A.
TITLE Transgenic bovine
JOURNAL Patent: US 5741957-A 37 21-APR-1998;
FEATURES
source
Location/Qualifiers
1..51
/organism="unknown"
/mol_type="unassigned DNA"

ORGANISM

Query Match 71.6%; Score 35.8; DB 6; Length 51;
Best Local Similarity 94.9%; Pred. No. 0.0063;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAACTTCTCATCTTACCTGTCCTGCTGCTGCTGCTGCT 39
|||||
Db 9 ATGAACTTCTTATCTCCTCACTGCTGCTGCTGCTGCTGCT 47
|||||

Search completed: October 1, 2005, 14:10:04
Job time : 860.407 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 11:36:51 ; Search time 296.018 Seconds
(without alignments)
999.897 Million cell updates/sec

Title: US-10-820-777-2

Perfect score:

Sequence: 1 atgaaacttctcatccttac.....gctgttgctgccagggttaac 50

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
						Probe	2 t
1	39	78.0	40	2	AAQ06046	AaQ06046	
2	39	78.0	82	2	AAQ14774	Cagein si	
3	39	78.0	303	2	AAQ14776	IGF-I und	
C 4	39	78.0	337	8	ABX47688	Bovine ES	
C 5	39	78.0	375	8	ABX45788	Bovine ES	
C 6	39	78.0	388	8	ABX45526	Bovine ES	
C 7	39	78.0	394	8	ABX43873	Bovine ES	
C 8	39	78.0	399	8	ABX49781	Bovine ES	
C 9	39	78.0	408	8	ABX40577	Bovine ES	
C 10	39	78.0	408	8	ABX49077	Bovine ES	
C 11	39	78.0	411	8	ABX44547	Bovine ES	
C 12	39	78.0	412	8	ABX47441	Bovine ES	
C 13	39	78.0	413	8	ABX39376	Bovine ES	
C 14	39	78.0	417	8	ABX47905	Bovine ES	
C 15	39	78.0	428	8	ABX48129	Bovine ES	
C 16	39	78.0	428	8	ABX38918	Bovine ES	
C 17	39	78.0	432	8	ABX35139	Bovine ES	
C 18	39	78.0	434	8	ABX46932	Bovine ES	
C 19	39	78.0	435	8	ABX36503	Bovine ES	
C 20	39	78.0	437	8	ABX49072	Bovine ES	

C	21	39	78.0	440	8	ABX35576	Abx35576	Bovine ES
C	22	39	78.0	445	8	ABX46229	Abx46229	Bovine ES
	23	39	78.0	450	8	ABX35547	Abx35547	Bovine ES
	24	39	78.0	1210	2	AAQ14051	Rennin ge	
	25	39	78.0	4438	2	AAQ14050	Alpha-S1-	
	26	37.4	74.8	384	8	ABX39403	Bovine ES	
C	27	37.4	74.8	413	8	ABX44318	Bovine ES	
	28	37.4	74.8	417	8	ABX36508	Bovine ES	
C	29	37.4	74.8	420	8	ABX35596	Bovine ES	
C	30	37.4	74.8	443	8	ABX49774	Bovine ES	
	31	35.8	71.6	51	3	AAZ87641	Linker GP	
	32	35.8	71.6	51	3	AAAS9939	Linker GP	
	33	35.8	71.6	51	4	AAC68336	DNA sequen	
C	34	35.8	71.6	51	10	ADE76694	Transgeni	
	35	34.2	68.4	45	2	AAQ14506	Alpha-S1-	
	36	34.2	68.4	60	2	AAQ06392	Bovine al	
	37	32.8	65.6	471	8	ABX40815	Bovine ES	
	38	32.6	65.2	268	8	ABX36736	Bovine ES	
C	39	32.6	65.2	415	8	ABX43653	Bovine ES	
	40	32.6	65.2	990	12	ADL313166	Human ste	
	41	32.4	64.8	39	2	AAT50866	Cattle al	
	42	31	62.0	349	8	ABX37209	Bovine ES	
C	43	31	62.0	668	6	AAD28314	IRES-bovi	
	44	31	62.0	668	6	AAD28275	IRES-bovi	
	45	31	62.0	668	12	ADM68975	IRES-Casse	

ALIGNMENTS

RESULT 1

AAQ06046
ID AAQ06046 standard; DNA; 40 BP.

AC AAQ06046;

25-MAR-2003 (revised)

DT 24-JAN-1991 (first entry)

Probe 2 to signal sequence of alpha S1 casein Chromosomal gene.

KW Bovine alpha S1 casein chromosomal gene; transgenic mice; ss.

OS Synthetic.

AA
PN
EP390592-A.

03-OCT-1990

XX
PF 30-MAR-1990: 90EP-00303445-XX
PP 31-MAR-1989. 89TP-00078574

XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (EXPE-) CENT INST EXPER ANIMALS.
PA (JIKK-) JIKKEN DORUTSII CHUO KENK.

XX
PT
Sekine S. Tto S. Katguki M:

XX
DR WPI: 1990-299492/40.

PT Prodn. of recombinant protein, esp. human pro:urokinase - from milk of transgenic animals using promoter of bovine alpha S1 casein chromosomal PT gene.

PS Example; Page 7; 55pp; English.

High molecular weight DNA from bovine liver was partially digested by *Sal*III and inserted into EMBL3 vector. Plaques were screened with two probes (#1 and #2). Probe 1 corresponds to the 5' non-coding region of bovine alpha S1 casein cDNA and a part of exon 1 of alpha S1 casein chromosomal gene. Probe 2 corresponds to part of the signal sequence region of bovine alpha S1 casein cDNA. One positive clone was obtained

CC from screening 150000 plaques. The promoter was then isolated from the
 CC gene. See also Q06045, Q06047-Q06049 and Q06392. (Updated on 25-MAR-2003
 CC to correct PA field.)

XX SQ Sequence 40 BP; 6 A; 11 C; 7 G; 16 T; 0 U; 0 Other;

Query Match 78.0%; Score 39; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACCTTCATCCTTACCTGCTGTGGCTGTGCT 39
 |||||

Db 1 ATGAACCTTCATCCTTACCTGCTGTGGCTGTGCT 39
 |||||

RESULT 2

AAQ14774
 ID AAQ14774 standard; DNA; 82 BP.

XX AC AAQ14774;

XX DT 25-MAR-2003 (revised)

XX DT 06-JAN-1992 (first entry)

XX DE Casein signal peptide - prorennin construct oligonucleotide CIIR1.

XX KW Prorennin; alpha-S1-casein gene; mammary gland; ss.

XX OS Synthetic.

XX PH Key Location/Qualifiers

FT sig_peptide 14..58

FT /*tag= a

FT /label= alpha-S1-casein-signal_peptide

FT CDS 59..77

FT /*tag= b

FT /label= prorennin

XX EP451823-A.

XX PD 16-OCT-1991.

XX PF 10-APR-1991; 91EP-00105702.

XX PR 11-APR-1990; 90DE-04011751.

XX PR 19-APR-1990; 90DE-04012526.

XX PA (CONE) CONSORTIUM ELEKTROCHEM IND.

XX PI Hartl P, Brem G;

XX DR WPI; 1991-304858/42.

XX PT Recombinant DNA constructs for expressing protein in milk - contg.
 XX specific mammary gland transcription control region and signal sequence,
 XX providing high yield and easy prod. recovery.

XX Example 3 (b); Page 9; 4lpp; German.

XX CC The rennin gene was ligated to the alpha-S1-casein promoter using the
 XX signal peptide sequence of the alpha-S1-casein gene. The constructs
 XX provide high yields of the protein with simple recovery from the milk.
 XX Activation of the gene occurs only in the mammary gland. See also
 CC AAQ14050-51, AAQ14774-77. (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 82 BP; 17 A; 24 C; 16 G; 25 T; 0 U; 0 Other;

Query Match 78.0%; Score 39; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACCTTCATCCTTACCTGCTGTGGCTGTGCT 39
 |||||

Db 14 ATGAACCTTCATCCTTACCTGCTGTGGCTGTGCT 52

RESULT 3

AAQ14776

XX ID AAQ14776 standard; DNA; 303 BP.

XX AC AAQ14776;

XX DT 25-MAR-2003 (revised)

XX DT 06-JAN-1992 (first entry)

XX DE IGF-I under alpha-S1-casein control regions.

XX KW Alpha-S1-casein gene; mammary gland; IGF-I; ss.

XX OS Synthetic.

XX PH Key Location/Qualifiers

FT sig_peptide 13..58

FT /*tag= a

FT /note= "derived from alpha-S1-casein gene"

FT mat_peptide 59..271

FT /*tag= b

FT /label= IGF-I

FT 3'UTR 272..303

FT /*tag= c

FT /note= "3' casein domain"

XX EP451823-A.

XX PD 16-OCT-1991.

XX PF 10-APR-1991; 91EP-00105702.

XX PR 11-APR-1990; 90DE-04011751.

XX PR 19-APR-1990; 90DE-04012526.

XX PA (CONE) CONSORTIUM ELEKTROCHEM IND.

XX PI Hartl P, Brem G;

XX DR WPI; 1991-304858/42.

XX PT Recombinant DNA constructs for expressing protein in milk - contg.
 XX specific mammary gland transcription control region and signal sequence,
 XX providing high yield and easy prod. recovery.

XX Example 3 (d); Page 11; 4lpp; German.

XX CC The constructs provide high yields of the protein with simple recovery
 XX from the milk. Activation of the gene occurs only in the mammary gland.
 CC See also AAQ14050-51, AAQ14774-77. (Updated on 25-MAR-2003 to correct PA
 CC field.)

XX SQ Sequence 303 BP; 45 A; 109 C; 90 G; 59 T; 0 U; 0 Other;

Query Match 78.0%; Score 39; DB 2; Length 303;

Best Local Similarity 100.0%; Pred. No. 9e-05;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACCTTCATCCTTACCTGCTGTGGCTGTGCT 39
 |||||

Db 14 ATGAACCTTCATCCTTACCTGCTGTGGCTGTGCT 52
 |||||

RESULT 4

ABX47688/c

ID ABX47688 standard; cDNA; 337 BP.

XX AC ABX47688;

XX DT 21-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #12853.
 XX AC
 XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX OS
 XX OS Bos Taurus.
 XX FN US2002137139-A1.
 XX PD 26-SEP-2002.
 XX XX
 XX PF 24-SEP-2001; 2001US-00960352.
 XX XX 12-JAN-1999; 99US-0115707P.
 XX PR 11-JAN-2000; 2000US-00480902.
 XX XX
 XX PA (BYAT/) BYATT J C.
 XX PA (MATH/) MATHIALAGAN N.
 XX PA (TAON/) TAO N.
 XX PA (WARR/) WARREN W C.
 XX XX
 XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX XX
 XX PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX XX
 XX PS Claim 2; SEQ ID NO 12853; 245pp; English.
 XX XX
 XX CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non-translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?docID=20020137139
 XX XX
 XX SQ Sequence 337 BP; 83 A; 68 C; 77 G; 108 T; 0 U; 1 Other;

Query Match 78.0%; Score 39; DB 8; Length 337;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGAACCTTCATCCTTACCTGCTGCTGCTGCTGCTGCT 39
 Db 304 ATGAACCTTCATCCTTACCTGCTGCTGCTGCTGCTGCT 266

RESULT 5
 ABX35788/c

ID XX ABX35788 standard; cDNA; 375 BP.
 XX AC
 XX XX ABX35788;
 XX DT 20-FEB-2003 (first entry)
 XX DE
 XX XX Bovine EST associated with lactation/muscle/fat deposition #953.
 XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX OS
 XX OS Bos Taurus.
 XX FN US2002137139-A1.
 XX PD 26-SEP-2002.
 XX XX
 XX PF 24-SEP-2001; 2001US-00960352.
 XX XX 12-JAN-1999; 99US-0115707P.
 XX PR 11-JAN-2000; 2000US-00480902.
 XX XX
 XX PA (BYAT/) BYATT J C.
 XX PA (MATH/) MATHIALAGAN N.
 XX PA (TAON/) TAO N.
 XX PA (WARR/) WARREN W C.
 XX XX
 XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX XX
 XX PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX XX
 XX PS Claim 2; SEQ ID NO 953; 245pp; English.
 XX XX
 XX CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non-translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?docID=20020137139
 XX XX
 XX SQ Sequence 375 BP; 97 A; 85 C; 77 G; 116 T; 0 U; 0 Other;
 Query Match 78.0%; Score 39; DB 8; Length 375;
 Best Local Similarity 100.0%; Pred. No. 9.4e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGAACCTTCATCCTTACCTGCTGCTGCTGCTGCTGCT 39
 |||||||||||||||||||||||||||||||||||||||||||

Db 368 ATGAACCTTCTCATCCTTACCTGCTCTGTGGCTGTGCT 330

RESULT 6
ABX45526
ID ABX45526 standard; cDNA; 388 BP.
XX
AC ABX45526;
XX
XX 21-FEB-2003 (first entry)
XX Bovine EST associated with lactation/muscle/fat deposition #10691.
XX
XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
XX Bos Taurus.
XX
XX US2002137139-A1.
XX
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
XX 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
XX (MATH/) MATHIALAGAN N.
XX (TAON/) TAO N.
XX (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 10691; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid; where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 388 BP; 113 A; 80 C; 91 G; 104 T; 0 U; 0 Other;
Query Match 78.0%; Score 39; DB 8; Length 388;

Best Local Similarity 100.0%; Pred. No. 9.5e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACCTTCTCATCCTTACCTGCTCTGTGGCTGTGCT 39
|||||
DB 54 ATGAACCTTCTCATCCTTACCTGCTCTGTGGCTGTGCT 92
|||||

RESULT 7
ABX43873/c
ID ABX43873 standard; cDNA; 394 BP.
XX
XX ABX43873;
XX
XX 21-FEB-2003 (first entry)
XX Bovine EST associated with lactation/muscle/fat deposition #9038.
XX
XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
XX Bos Taurus.
XX
XX US2002137139-A1.
XX
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
XX 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
XX (MATH/) MATHIALAGAN N.
XX (TAON/) TAO N.
XX (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 9038; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid; where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX


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CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 394 BP; 109 A; 92 C; 82 G; 111 T; 0 U; 0 Other;

Query Match      78.0%; Score 39; DB 8; Length 394;
Best Local Similarity 100.0%; Pred. No. 9.5e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGAAGACTTCTCATCCTTACCTGCTGCTTGTGGCTGTGCT 39
    |||||
Db 341 ATGAAGACTTCTCATCCTTACCTGCTGCTTGTGGCTGTGCT 303

RESULT 8
ABX49781/c
ID ABX49781 standard; cDNA; 399 BP.
AC ABX49781;
XX
XX 21-FEB-2003 (first entry)
XX
XX Bovine EST associated with lactation/muscle/fat deposition #14946.
XX
XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
XX Bos Taurus.
XX
XX US2002137139-A1.
XX
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
XX
XX 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
XX (MATH/) MATHIALAGAN N.
XX (TAON/) TAO N.
XX (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
XX deposition, useful for genome mapping, gene identification and analysis,
XX cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 14946; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
XX lactation or muscle and fat deposition (designated LMFD), derived from
XX cattle, and the LMFD nucleic acid can specifically hybridize to a second
XX nucleic acid molecule comprising any of 15112 nucleotide sequences,
XX appearing as ABX34836-ABX49947, or complements of them. Also included are
XX ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX acid linked to a promoter and a 3' non-translated sequence that
XX functions in the cell to cause termination of transcription and addition
XX of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX (2) determining a level or pattern of a molecule in a bovine cell or
XX tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX of the 15112 nucleic acid sequences or its complement or fragment) with a
XX complementary nucleic acid molecule obtained from the bovine cell or
XX tissue, where hybridization between the marker nucleic acid and the
XX complementary nucleic acid permits the detection of the molecule; and (b)
XX It is useful for genome mapping, gene identification and analysis, cattle

```

```

CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 399 BP; 107 A; 93 C; 83 G; 116 T; 0 U; 0 Other;

Query Match      78.0%; Score 39; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 9.5e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGAAGACTTCTCATCCTTACCTGCTGCTTGTGGCTGTGCT 39
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Db 353 ATGAAGACTTCTCATCCTTACCTGCTGCTTGTGGCTGTGCT 315

RESULT 9
ABX40577/c
ID ABX40577 standard; cDNA; 408 BP.
AC ABX40577;
XX
XX 20-FEB-2003 (first entry)
XX
XX Bovine EST associated with lactation/muscle/fat deposition #5742.
XX
XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
XX Bos Taurus.
XX
XX US2002137139-A1.
XX
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
XX
XX 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
XX (MATH/) MATHIALAGAN N.
XX (TAON/) TAO N.
XX (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
XX deposition, useful for genome mapping, gene identification and analysis,
XX cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 5742; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
XX lactation or muscle and fat deposition (designated LMFD), derived from
XX cattle, and the LMFD nucleic acid can specifically hybridize to a second
XX nucleic acid molecule comprising any of 15112 nucleotide sequences,
XX appearing as ABX34836-ABX49947, or complements of them. Also included are
XX ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX acid linked to a promoter and a 3' non-translated sequence that
XX functions in the cell to cause termination of transcription and addition
XX of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX (2) determining a level or pattern of a molecule in a bovine cell or
XX tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX of the 15112 nucleic acid sequences or its complement or fragment) with a
XX complementary nucleic acid molecule obtained from the bovine cell or
XX tissue, where hybridization between the marker nucleic acid and the
XX complementary nucleic acid permits the detection of the molecule; and (b)
XX complementary nucleic acid permits the detection of the molecule; and (b)

```

CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX
 SQ Sequence 408 BP; 109 A; 93 C; 85 G; 121 T; 0 U; 0 Other;
 Query Match 78.0%; Score 39; DB 8; Length 408;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAACTTCTCATCTTACCTGCTGTGTGGCTGTGCT 39
 Db 362 ATGAACTTCTCATCTTACCTGCTGTGTGGCTGTGCT 324
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 ABX49077/C
 ID ABX49077 standard; cDNA; 408 BP.
 XX AC ABX49077;
 XX 21-FEB-2003 (first entry)
 XX Bovine EST associated with lactation/muscle/fat deposition #14242.
 XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX Bos Taurus.
 XX US2002137139-A1.
 XX 26-SEP-2002.
 XX 24-SEP-2001; 2001US-00960352.
 XX 12-JAN-1999; 99US-0115707P.
 PR 11-JAN-2000; 2000US-00480902.
 XX (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 DR WPI; 2003-110599/10.
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX Claim 2; SEQ ID NO 14242; 245pp; English.
 XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non-translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or

CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX
 SQ Sequence 408 BP; 105 A; 88 C; 80 G; 135 T; 0 U; 0 Other;
 Query Match 78.0%; Score 39; DB 8; Length 408;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAACTTCTCATCTTACCTGCTGTGTGGCTGTGCT 39
 Db 327 ATGAACTTCTCATCTTACCTGCTGTGTGGCTGTGCT 289
 RESULT 11
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 ID ABX44547 standard; cDNA; 411 BP.
 XX AC ABX44547;
 XX 21-FEB-2003 (first entry)
 XX Bovine EST associated with lactation/muscle/fat deposition #9712.
 XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX Bos Taurus.
 XX US2002137139-A1.
 XX 26-SEP-2002.
 XX 24-SEP-2001; 2001US-00960352.
 XX 12-JAN-1999; 99US-0115707P.
 PR 11-JAN-2000; 2000US-00480902.
 XX (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 DR WPI; 2003-110599/10.
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX Claim 2; SEQ ID NO 9712; 245pp; English.
 XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are

(1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 1512 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 1512 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139

XX	Sequence	411 BP; 88 A; 117 C; 102 G; 104 T; 0 U; 0 Other;
SQ	Query Match	78.0%; Score 39; DB 8; Length 411;
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	Matches 39; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT 39
|||
Db 253 ATGAAACTTCTCATCCTTACCTGTCTTGTGGCTGTTGCT 291

RESULT 12	
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ID ABX47441 standard; cDNA; 412 BP.	
XX	
AC ABX47441;	
XX	
DT 21-FEB-2003 (first entry)	
XX	
DE Bovine EST associated with lactation/muscle/fat deposition #I2606.	
XX	
DE Bovine; ss; EST; expressed sequence tag; lactation; LMPD;	
KM muscle deposition; fat deposition; genome mapping; gene identification;	
KW gene analysis; cattle breeding.	
XX	
OS Bos Taurus.	
XX	
PN US2002137139-A1.	
XX	
PD 26-SEP-2002.	
XX	
PF 24-SEP-2001; 2001US-00960352.	
XX	
PR 12-JAN-1999; 99US-0115707P.	
PR 11-JAN-2000; 2000US-00480902.	
XX	
PA (BYAT/) BYATT J C.	
PA (MATH/) MATHIALAGAN N.	
PA (TAON/) TAO N.	
PA (WARR/) WARREN W C.	
XX	
PI Byatt JC, Mathialagan N, Tao N, Warren WC;	
DR WPI; 2003-110599/10.	
XX	
PT New nucleic acid associated with lactation, and muscle and fat	
PT deposition, useful for genome mapping, gene identification and analysis	
PT cattle breeding, or for genetically improving cattle.	
XX	
PS Claim 2; SEQ ID NO 12606; 245pp; English.	
XX	

PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.

XX
 PS Claim 2; SEQ ID NO 4541; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 1512 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 1512 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 1512 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139

XX
 SQ Sequence 413 BP; 102 A; 87 C; 76 G; 148 T; 0 U; 0 Other;

Query Match 78.0%; Score 39; DB 8; Length 413;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACTTCTCATCTTACCTGCTGTGTGGCTGTGCT 39
 |||||
 Db 362 ATGAACTTCTCATCTTACCTGCTGTGTGGCTGTGCT 324

RESULT 14
 ABX47905/c
 ID ABX47905 standard; cDNA; 417 BP.

XX
 AC ABX47905;

XX
 DT 21-FEB-2003 (first entry)

XX
 DE Bovine EST associated with lactation/muscle/fat deposition #13070.

XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.

XX
 OS Bos Taurus.

XX
 PN US2002137139-A1.

XX
 PD 26-SEP-2002.

XX
 PF 24-SEP-2001; 2001US-00960352.

XX
 PR 12-JAN-1999; 99US-0115707P.

XX
 PR 11-JAN-2000; 2000US-00480902.

XX
 PA (BYAT/) BYATT J C.

XX
 PA (MATH/) MATHIALAGAN N.

XX
 PA (TAON/) TAO N.

XX
 PA (WARR/) WARREN W C.

XX

PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.

XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.

XX Claim 2; SEQ ID NO 13070; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 1512 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 1512 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 1512 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139

XX
 SQ Sequence 417 BP; 111 A; 92 C; 89 G; 125 T; 0 U; 0 Other;

Query Match 78.0%; Score 39; DB 8; Length 417;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACTTCTCATCTTACCTGCTGTGTGGCTGTGCT 39
 |||||
 Db 362 ATGAACTTCTCATCTTACCTGCTGTGTGGCTGTGCT 324

RESULT 15

ABX48129

ID ABX48129 standard; cDNA; 428 BP.

XX
 AC ABX48129;

XX
 DT 21-FEB-2003 (first entry)

XX
 DE Bovine EST associated with lactation/muscle/fat deposition #13294.

XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.

XX
 OS Bos Taurus.

XX
 PN US2002137139-A1.

XX
 PD 26-SEP-2002.

XX
 PF 24-SEP-2001; 2001US-00960352.

XX
 PR 12-JAN-1999; 99US-0115707P.

XX
 PR 11-JAN-2000; 2000US-00480902.

XX

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 13:13:06 ; Search time 2320.8 Seconds
(without alignments)
820.069 Million cell updates/sec

Title: US-10-820-777-2

Perfect score: 50

Sequence: 1 atgaacctctcattccttac.....gctgttgctgccaggttaac 50

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_ges1:*

9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	80.0	357	4	BG692772 342586 BA
2	39	78.0	103	2	B845866 232673 BA
3	39	78.0	105	2	B8479124 163696 BA
4	39	78.0	108	2	B8477105 160562 BA
5	39	78.0	110	2	BF231307 253648 BA
6	39	78.0	113	2	B8589286 195358 BA
7	39	78.0	114	2	B8481164 166493 BA
8	39	78.0	119	4	BG694048 344882 BA
9	39	78.0	130	2	B8486332 172970 BA
10	39	78.0	132	2	BF230751 252603 BA
11	39	78.0	132	4	BG690967 339938 BA
12	39	78.0	134	2	B8479391 163981 BA
13	39	78.0	134	2	B8486475 174442 BA
14	39	78.0	135	2	B8487072 175631 BA
15	39	78.0	142	2	B8476912 160364 BA
16	39	78.0	154	4	BG690375 338890 BA
17	39	78.0	155	4	BG693677 344158 BA
18	39	78.0	156	2	B8477525 161268 BA
19	39	78.0	156	2	B8478556 162863 BA
20	39	78.0	156	2	B8487058 175608 BA
21	39	78.0	158	2	B8486465 174414 BA
22	39	78.0	158	4	BG694067 344954 BA
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24	39	78.0	160	2	B8485392 172409 BA

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28	39	78.0	165	2	B8589229
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38	39	78.0	173	4	BG693529
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41	39	78.0	176	2	BE8486101
42	39	78.0	177	2	BE8483593
43	39	78.0	177	2	BE8486179
44	39	78.0	178	2	BE8477162
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ALIGNMENTS

RESULT 1
LOCUS BG692772 357 bp mRNA linear EST 27-MAR-2003
DEFINITION 342586 BARC 5BOV Bos taurus cdna 5', mRNA sequence.
ACCESSION BG692772
VERSION BG692772.1 GI:13934592
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 357)
AUTHORS Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
Connor, E.E., Cho, J., Sulfana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
TITLE Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
JOURNAL Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE 22135956
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psa.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
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Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

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Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 52 ATGAAACTTCTCATCCTTACTGCTGTGTGGCTGTGCTG 91

RESULT 2
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LOCUS      232673 BARC 5BOV Bos taurus cDNA 5', mRNA sequence. EST 27-MAR-2003
DEFINITION
ACCESSION BE845866
VERSION    BE845866.1 GI:10282690
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE  1 (bases 1 to 103)
AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
TITLE     Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
JOURNAL    Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE    22135956
PUBMED     12140684
COMMENT    Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
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Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

FEATURES
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Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

ORIGIN
Query Match      78.0%; Score 39; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTCATCCTTACTGCTGTGTGGCTGTGCT 39
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Db 51 ATGAAACTTCTCATCCTTACTGCTGTGTGGCTGTGCT 89

RESULT 4
BE477105
LOCUS      160562 BARC 5BOV Bos taurus cDNA 5', mRNA sequence. EST 27-MAR-2003
DEFINITION
ACCESSION BE477105
VERSION    BE477105.1 GI:9596575
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE  1 (bases 1 to 108)
AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
and Quackenbush,J.
TITLE     Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
JOURNAL    Mamm. Genome 13 (7), 373-379 (2002)

```



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MEDLINE      22135956
PUBMED      12140684
COMMENT
Contact: Sonstegard TS
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Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 1 row: B column: 20
Seq primer: ATTTAGTGACACTATAG.

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        Location/Qualifiers
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                /mol_type="mRNA"
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                /tissue_type="pooled"
                /lab_host="DH10B"
                /clone_lib="BARC 5BOV"
                /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
                Library made from pooled mRNA isolated from mammary
                tissues at eight physiological, developmental, and disease
                states."

ORIGIN
Query Match      78.0%; Score 39; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  ATGAACTTCTCATCTTACCTGCTGTGGCTGTGCT 39
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RESULT 5
BF231307
LOCUS      BF231307
DEFINITION 253648 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BF231307
VERSION     BF231307.1 GI:11170184
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE  1 (bases 1 to 110)
            Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
            Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
            and Quackenbush, J.
            Analysis of bovine mammary gland EST and functional annotation of
            the Bos taurus gene index
            Mamm. Genome 13 (7), 373-379 (2002)
            22135956
            PUBMED 12140684
COMMENT    Contact: Sonstegard TS
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            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTCCTCAGTCACGACG
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                /tissue_type="pooled"
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                /clone_lib="BARC 5BOV"
                /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
                Library made from pooled mRNA isolated from mammary
                tissues at eight physiological, developmental, and disease
                states."

ORIGIN
Query Match      78.0%; Score 39; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  ATGAACTTCTCATCTTACCTGCTGTGGCTGTGCT 39
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Db   45 ATGAACTTCTCATCTTACCTGCTGTGGCTGTGCT 83
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RESULT 6
BE589286
LOCUS      BE589286
DEFINITION 195358 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE589286
VERSION     BE589286.1 GI:9842325
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE  1 (bases 1 to 113)
            Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
            Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
            and Quackenbush, J.
            Analysis of bovine mammary gland EST and functional annotation of
            the Bos taurus gene index
            Mamm. Genome 13 (7), 373-379 (2002)
            22135956
            PUBMED 12140684
COMMENT    Contact: Sonstegard TS
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            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTCCTCAGTCACGACG
            Plate: 120 row: D column: 7
            Seq primer: ATTTAGTGACACTATAG.

FEATURES
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                /clone_lib="BARC 5BOV"
                /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
                Library made from pooled mRNA isolated from mammary
                tissues at eight physiological, developmental, and disease
                states."

ORIGIN

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Query Match      78.0%; Score 39; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 45 ATGAAACTTCTCATCTTACTGCTGTTGGCTGTTGCT 83

RESULT 7
BE481164
LOCUS      BE481164          114 bp mRNA linear EST 27-MAR-2003
DEFINITION 156493 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE481164
VERSION    BE481164.1 GI:9600697
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
           Bovinae; Bos.
REFERENCE  1 (bases 1 to 114)
AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
           Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
           and Quackenbush,J.
TITLE     Analysis of bovine mammary gland EST and functional annotation of
           the Bos taurus gene index
JOURNAL   Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE   22135956
PUBMED    12140684
COMMENT   Contact: Sonstegard TS
           USDA, ARS, Beltsville Agricultural Research Center
           Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
           Tel: 301 504 8416
           Fax: 301 504 8414
           Email: tads@psi.barc.usda.gov
           Single pass sequencing. Bases called and alt trimmed with phred
           v0.980904.e. Vector identified by cross_match with the -minscore 18
           and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 9 row: D column: 5
Seq primer: ATTTAGTGACACTATAG.
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           /mol_type="mRNA"
           /db_xref="taxon:9913"
           /tissue_type="pooled"
           /lab_host="DH10B"
           /clone_lib="BARC 5BOV"
           /notes="Vector: pCMV SPOT6; Site 1: NotI; Site 2: SalI;
           Library made from pooled mRNA isolated from mammary
           tissues at eight physiological, developmental, and disease
           states."

FEATURES
source
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 9 row: D column: 5
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
1. .114
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
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/clone_lib="BARC 5BOV"
/notes="Vector: pCMV SPOT6; Site 1: NotI; Site 2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

ORIGIN
Query Match      78.0%; Score 39; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTCATCTTACTGCTGTTGGCTGTTGCT 39
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Db 49 ATGAAACTTCTCATCTTACTGCTGTTGGCTGTTGCT 87

RESULT 8
BG694048
LOCUS      BG694048          119 bp mRNA linear EST 27-MAR-2003
DEFINITION 344882 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BG694048
VERSION    BG694048.1 GI:13935868

Query Match      78.0%; Score 39; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTCATCTTACTGCTGTTGGCTGTTGCT 39
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Db 49 ATGAAACTTCTCATCTTACTGCTGTTGGCTGTTGCT 87

RESULT 8
BG694048
LOCUS      BG694048          119 bp mRNA linear EST 27-MAR-2003
DEFINITION 344882 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BG694048
VERSION    BG694048.1 GI:13935868

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KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
           Bovinae; Bos.
REFERENCE  1 (bases 1 to 119)
AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
           Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
           and Quackenbush,J.
TITLE     Analysis of bovine mammary gland EST and functional annotation of
           the Bos taurus gene index
JOURNAL   Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE   22135956
PUBMED    12140684
COMMENT   Contact: Sonstegard TS
           USDA, ARS, Beltsville Agricultural Research Center
           Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
           Tel: 301 504 8416
           Fax: 301 504 8414
           Email: tads@psi.barc.usda.gov
           Single pass sequencing. Bases called and alt trimmed with phred
           v0.980904.e. Vector identified by cross_match with the -minscore 18
           and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 31 row: B column: 1
Seq primer: ATTTAGTGACACTATAG.
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           /lab_host="DH10B"
           /clone_lib="BARC 5BOV"
           /notes="Vector: pCMV SPOT6; Site 1: NotI; Site 2: SalI;
           Library made from pooled mRNA isolated from mammary
           tissues at eight physiological, developmental, and disease
           states."

ORIGIN
Query Match      78.0%; Score 39; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTCATCTTACTGCTGTTGGCTGTTGCT 39
    |||||||
Db 20 ATGAAACTTCTCATCTTACTGCTGTTGGCTGTTGCT 58

RESULT 9
BE486332
LOCUS      BE486332          130 bp mRNA linear EST 27-MAR-2003
DEFINITION 173970 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE486332
VERSION    BE486332.1 GI:9605802
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
           Bovinae; Bos.
REFERENCE  1 (bases 1 to 130)
AUTHORS   Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
           Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
           and Quackenbush,J.
TITLE     Analysis of bovine mammary gland EST and functional annotation of
           the Bos taurus gene index
JOURNAL   Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE   22135956
PUBMED    12140684

```

COMMENT

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 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCAGTCACGACG
 Plate: 129 row: G column: 9
 Seq primer: ATTTAGTGACACTATAG.
 Location/Qualifiers

FEATURES

source

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 /db_xref="taxon:9913"
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 /clone_lib="BARC 5BOV"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

ORIGIN

Query Match 78.0%; Score 39; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.0039;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCATCTTACCTTACCTGCTTGTGGCTGTGCT 39

Db 49 ATGAACTTCATCTTACCTTACCTGCTTGTGGCTGTGCT 87

RESULT 10

BF230751 132 bp mRNA linear EST 27-MAR-2003
 LOCUS
 DEFINITION 252603 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BF230751
 VERSION BF230751.1 GI:11169055
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE

AUTHORS

1 (bases 1 to 132)
 Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
 Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
 and Quackenbush, J.

Analysis of bovine mammary gland EST and functional annotation of
 the Bos taurus gene index
 Mamm. Genome 13 (7), 373-379 (2002)

JOURNAL

MEDLINE

PUBMED

12140684

COMMENT

Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
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 Fax: 301 504 8414

Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCAGTCACGACG
 Plate: 109 row: M column: 24
 Seq primer: ATTTAGTGACACTATAG.
 Location/Qualifiers

FEATURES

Query Match 78.0%; Score 39; DB 4; Length 132;
 Best Local Similarity 100.0%; Pred. No. 0.0039;

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 /clone_lib="BARC 5BOV"
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 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

ORIGIN

Query Match 78.0%; Score 39; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 0.0039;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCATCTTACCTTACCTGCTTGTGGCTGTGCT 39

Db 51 ATGAACTTCATCTTACCTTACCTGCTTGTGGCTGTGCT 89

RESULT 11

BG690967 132 bp mRNA linear EST 27-MAR-2003
 LOCUS
 DEFINITION 339938 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BG690967
 VERSION BG690967.1 GI:13932787
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE

AUTHORS

1 (bases 1 to 132)
 Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
 Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
 and Quackenbush, J.

Analysis of bovine mammary gland EST and functional annotation of
 the Bos taurus gene index
 Mamm. Genome 13 (7), 373-379 (2002)

JOURNAL

MEDLINE

PUBMED

12140684

COMMENT

Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCAGTCACGACG
 Plate: 100 row: J column: 1
 Seq primer: ATTTAGTGACACTATAG.
 Location/Qualifiers

FEATURES

source

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 /db_xref="taxon:9913"
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 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

ORIGIN

Query Match 78.0%; Score 39; DB 4; Length 132;
 Best Local Similarity 100.0%; Pred. No. 0.0039;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTACCTTACCTGCTGCTGCTGCTGCT 39
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 Db 32 ATGAAACTTCTACCTTACCTGCTGCTGCTGCTGCT 70
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RESULT 12

BE479391
 LOCUS 163981 BARC 5BOV Bos taurus cDNA 5', mRNA linear EST 27-MAR-2003
 DEFINITION
 ACCESSION BE479391
 VERSION BE479391.1 GI:9598861
 KEYWORDS
 SOURCE EST.
 ORGANISM Bos taurus (cow)

ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 134)
 AUTHORS Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
 Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
 and Quackenbush,J.

TITLE Analysis of bovine mammary gland EST and functional annotation of
 the Bos taurus gene index

JOURNAL Mamm. Genome 13 (7), 373-379 (2002)
 MEDLINE 22135956
 PUBMED 12140684
 COMMENT

Contact: Sonstegard TS
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 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCACGACG
 Plate: 140 row: K column: 13
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers

FEATURES
 source

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 /lab_host="DH10B"
 /clone_lib="BARC 5BOV"

/notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

ORIGIN

Query Match 78.0%; Score 39; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 0.0039;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTACCTTACCTGCTGCTGCTGCTGCT 39
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 Db 55 ATGAAACTTCTACCTTACCTGCTGCTGCTGCTGCT 93
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RESULT 13

BE486475
 LOCUS 174442 BARC 5BOV Bos taurus cDNA 5', mRNA linear EST 27-MAR-2003
 DEFINITION
 ACCESSION BE486475
 VERSION BE486475.1 GI:9606008
 KEYWORDS
 SOURCE EST.
 ORGANISM Bos taurus (cow)

ORGANISM

Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE
AUTHORS

1 (bases 1 to 134)
 Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
 Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
 and Quackenbush,J.

TITLE Analysis of bovine mammary gland EST and functional annotation of
 the Bos taurus gene index

JOURNAL Mamm. Genome 13 (7), 373-379 (2002)
 MEDLINE 22135956
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 COMMENT

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 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCACGACG
 Plate: 128 row: K column: 1
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers

FEATURES
 source

1..134
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 /tissue_type="pooled"
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/notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

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 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14

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 DEFINITION
 ACCESSION BE487072
 VERSION BE487072.1 GI:9606605
 KEYWORDS
 SOURCE EST.
 ORGANISM Bos taurus (cow)

ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 135)
 AUTHORS Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P.,
 Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D.
 and Quackenbush,J.

TITLE Analysis of bovine mammary gland EST and functional annotation of
 the Bos taurus gene index

JOURNAL Mamm. Genome 13 (7), 373-379 (2002)
 MEDLINE 22135956
 PUBMED 12140684
 COMMENT

Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414

Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG

Plate: 125 row: L column: 14

Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers

1. .135

/organism="Bos taurus"

/mol_type="mRNA"

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/tissue_type="pooled"

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/clone_lib="BARC 5BOV"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

FEATURES

source

ORIGIN

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DB 33 ATGAAACTTCTCATCTTACTGCTGCTTGTGGCTGTGCT 71
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Search completed: October 1, 2005, 15:37:40
Job time : 2321.8 secs

ORIGIN

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RESULT 15

BE476912

LOCUS

160364 BARC 5BOV Bos taurus cDNA 5', mRNA sequence. EST 27-MAR-2003

DEFINITION

BE476912

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos.

1 (bases 1 to 142)

Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,

Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.

and Quackenbush, J.

Analysis of bovine mammary gland EST and functional annotation of

the Bos taurus gene index

Mamm. Genome 13 (7), 373-379 (2002)

22135956

12140684

CONTACT: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414

Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG

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Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers

1. .142

/organism="Bos taurus"

FEATURES

source

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/tissue_type="pooled"

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/clone_lib="BARC 5BOV"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled mRNA isolated from mammary

tissues at eight physiological, developmental, and disease

states."

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 13:15:56 ; Search time 88.4956 Seconds
(without alignments)
924.496 Million cell updates/sec

Title: US-10-820-777-2

Perfect score: 50

Sequence: 1 atgaactctctcctcttac.....gctgttgctgccagggttaac 50

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	35.8	71.6	51	1	US-08-154-019-37
3	35.8	71.6	51	1	US-08-461-333-37
4	35.8	71.6	51	3	US-08-464-167-37
5	35.8	71.6	51	3	US-09-158-313-37
6	35.8	71.6	51	3	US-08-476-798-37
7	32.6	65.2	981	4	US-09-949-016-2353
8	32.6	65.2	990	4	US-09-976-594-895
9	32.6	65.2	19480	4	US-09-949-016-14095
10	32.4	64.8	39	2	US-08-723-306-12
11	32.4	64.8	39	5	PCT-US96-10041-12
12	28	56.0	38	2	US-08-723-306-16
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23	26.6	53.2	63926	4	US-09-949-016-16473
24	26.6	53.2	64626	4	US-09-949-016-12011
25	26.2	52.4	341	4	US-09-621-976-13459
26	26.2	52.4	708	1	US-08-078-090-24
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30	26.2	52.4	1065	1	US-08-249-584-1	Sequence 1, Appli
31	26.2	52.4	1065	1	US-08-734-792-1	Sequence 1, Appli
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41	25.2	50.4	11093	2	US-08-723-306-5	Sequence 5, Appli
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ALIGNMENTS

RESULT 1

US-08-545-573A-40

; Sequence 40, Application US/08545573A

; Patent No. 6495344

; GENERAL INFORMATION:

; APPLICANT: Carr, No. 64953441 Gordon

; APPLICANT: Mann, Nicholas Harold

; TITLE OF INVENTION: Phenylalanine-Free Protein and DNA Coding

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/545,573A

; FILING DATE: 16-JAN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB94/01046

; FILING DATE: 16-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9310472.7

; FILING DATE: 20-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Liebeschuetz, Joe

; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 016994-011900US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1123 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Bos taurus

; FEATURE:

; NAME/KEY: -

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; NAME/KEY: sig_peptide
; LOCATION: 64..108
; OTHER INFORMATION: /note= "bovine alpha-s1-casein signal"
; OTHER INFORMATION: peptide"
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; OTHER INFORMATION: /note= "bovine alpha-s1-casein"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64..708
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; OTHER INFORMATION: precursor"
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Db 64 ATGAACCTTCTCATCTTACCTGTCTGTGGCTGTGCT 102
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; Sequence 37, Application US/08154019
; Patent No. 5633076
; GENERAL INFORMATION:
; APPLICANT: Deboer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krimpenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,019
; FILING DATE: 16-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/461,333
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
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; NAME: Liebeschultz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc feature
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US-08-154-019-37
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; Sequence 37, Application US/08461333
; Patent No. 5741957
; GENERAL INFORMATION:
; APPLICANT: Deboer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krimpenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,333
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschultz, Joe O.
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REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2
OTHER INFORMATION: /note= "Overhang"
US-08-461-333-37

Query Match 71.6%; Score 35.8; DB 1; Length 51;
Best Local Similarity 94.9%; Pred. No. 5.2e-05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 9 ATGAACTTCTTATCTCCTCACTGTCTTGTGGCTGTGCT 47

RESULT 4

US-08-464-167-37
Sequence 37, Application US/08464167
Patent No. 6013857
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,167
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 16994-003124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2
OTHER INFORMATION: /note= "Overhang"
US-08-464-167-37

Query Match 71.6%; Score 35.8; DB 3; Length 51;
Best Local Similarity 94.9%; Pred. No. 5.2e-05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 9 ATGAACTTCTTATCTCCTCACTGTCTTGTGGCTGTGCT 47

RESULT 5

US-09-158-313-37
Sequence 37, Application US/09158313
Patent No. 6066725
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,313
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc feature
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; OTHER INFORMATION: /note= "Overhang"
US-09-158-313-37

Query Match 71.6%; Score 35.8; DB 3; Length 51;
Best Local Similarity 94.9%; Pred. No. 5.2e-05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAACTTCTCATCCTTACCTGTCCTGTGTGGCTGTTGCT 39
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Db 9 ATGAACTTCTTATCCTCACCTGTCCTGTGTGGCTGTTGCT 47
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RESULT 6
US-08-476-798-37
; Sequence 37, Application US/08476798
; Patent No. 6140552
; GENERAL INFORMATION:
; APPLICANT: Deboer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krimpenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,798
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003125
; TELECOMMUNICATION INFORMATION:

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; SEQ ID NO 895
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 998930.1
; NAME/KEY: unsaure
; LOCATION: 984
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-895

Query Match 65.2%; Score 32.6; DB 4; Length 990;
Best Local Similarity 89.7%; Pred. No. 0.0025;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAACCTTCTCATCTTACCTGCTTGTGGCTGTTGCT 39
Db 50 ATGAGGCTTCTCATCTTACCTGCTTGTGGCTGTTGCT 88

RESULT 9

US-09-949-016-14095
; Sequence 14095, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14095
; LENGTH: 19480
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14095

Query Match 65.2%; Score 32.6; DB 4; Length 19480;
Best Local Similarity 89.7%; Pred. No. 0.0065;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAACCTTCTCATCTTACCTGCTTGTGGCTGTTGCT 39
Db 3476 ATGAGGCTTCTCATCTTACCTGCTTGTGGCTGTTGCT 3514

RESULT 10

US-08-723-306-12/c
; Sequence 12, Application US/08723306
; Patent No. 5856178
; GENERAL INFORMATION:
; APPLICANT: White PhD, Kenneth
; APPLICANT: Morrey PhD, John
; APPLICANT: Reed, William
; TITLE OF INVENTION: Cassette for Expression of Lytic
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Trask Britt and Rossa
; STREET: P.O. Box 2550
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: USA
; ZIP: 84110

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,306
; FILING DATE:

CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweigert PhD, Susan E
; REGISTRATION NUMBER: 36,289
; REFERENCE/DOCKET NUMBER: 2549
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 8015321922
; TELEFAX: 8015319168

; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: not relevant
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Downstream primer for Bos
; DESCRIPTION: taurus alpha-S1-casein 5' regulatory region including
; DESCRIPTION: restriction site linker"
; HYPOTHETICAL: YES
US-08-723-306-12

Query Match 64.8%; Score 32.4; DB 2; Length 39;
Best Local Similarity 97.1%; Pred. No. 0.0011;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTTACCTGCTTGTGGCTGTTGCTGCCAG 44
Db 39 TCATCCTTACCTGCTTGTGGCTGTTGCTGCTAG 6

RESULT 11

PCT-US96-10041-12/c
; Sequence 12, Application PC/TUS9610041
; GENERAL INFORMATION:
; APPLICANT: White PhD, Kenneth
; APPLICANT: Morrey PhD, John
; APPLICANT: Reed, William
; TITLE OF INVENTION: Cassette for Expression of Lytic
; TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Trask Britt and Rossa
; STREET: P.O. Box 2550
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: USA
; ZIP: 84110

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10041
; FILING DATE:

CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweigert PhD, Susan E
; REGISTRATION NUMBER: 36,289
; REFERENCE/DOCKET NUMBER: 2549
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 8015321922
; TELEFAX: 8015319168
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Downstream primer for Bos
; DESCRIPTION: taurus alpha-S1-casein 5' regulatory region including
; DESCRIPTION: restriction site linker"
; HYPOTHETICAL: YES
PCT-US96-10041-12

Query Match 64.8%; Score 32.4; DB 5; Length 39;
Best Local Similarity 97.1%; Pred. No. 0.0011;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCATCCTTACCTGCTCTGTGGCTGTGCTGCAG 44
|||||
Db 39 TCATCCTTACCTGCTCTGTGGCTGTGCTGCTAG 6

RESULT 12
US-08-723-306-16/c
; Sequence 16, Application US/08723306
; Patent No. 5856178
; GENERAL INFORMATION:
; APPLICANT: White PhD, Kenneth
; APPLICANT: Morrey PhD, John
; APPLICANT: Reed, William
; TITLE OF INVENTION: Cassette for Expression of Lytic
; TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Trask Britt and Rossa
; STREET: P.O. Box 2550
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: USA
; ZIP: 84110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,306
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweigert PhD, Susan E
; REGISTRATION NUMBER: 36,289
; REFERENCE/DOCKET NUMBER: 2549
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 8015321922
; TELEFAX: 8015319168
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Downstream primer for Capra
; DESCRIPTION: hircus beta lactoglobulin 5' promoter region including
; DESCRIPTION: restriction site linker"
; HYPOTHETICAL: YES
US-08-723-306-16

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Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCTTACCTGCTCTGTGGCTGTGCG 38
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Db 11 TCATCCTTACCTGCTCTGTGGCTGTGCG 38

RESULT 14
US-09-028-551-7
; Sequence 7, Application US/09028551
; Patent No. 6528699
; GENERAL INFORMATION:
; APPLICANT: Harry Meade et al.
; TITLE OF INVENTION: TRANSGENICALLY PRODUCED
; TITLE OF INVENTION: NON-SECRETED PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
```

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Db 38 TCATCCTTACCTGCTCTGTGGCTGTGCG 11

RESULT 13
PCT-US96-10041-16/c
; Sequence 16, Application PC/TUS9610041
; GENERAL INFORMATION:
; APPLICANT: White PhD, Kenneth
; APPLICANT: Morrey PhD, John
; APPLICANT: Reed, William
; TITLE OF INVENTION: Cassette for Expression of Lytic
; TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Trask Britt and Rossa
; STREET: P.O. Box 2550
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: USA
; ZIP: 84110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10041
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweigert PhD, Susan E
; REGISTRATION NUMBER: 36,289
; REFERENCE/DOCKET NUMBER: 2549
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 8015321922
; TELEFAX: 8015319168
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Downstream primer for Capra
; DESCRIPTION: hircus beta lactoglobulin 5' promoter region including
; DESCRIPTION: restriction site linker"
; HYPOTHETICAL: YES
PCT-US96-10041-16

Query Match 56.0%; Score 28; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TCATCCTTACCTGCTCTGTGGCTGTGCG 38
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Db 38 TCATCCTTACCTGCTCTGTGGCTGTGCG 11

RESULT 14
US-09-028-551-7
; Sequence 7, Application US/09028551
; Patent No. 6528699
; GENERAL INFORMATION:
; APPLICANT: Harry Meade et al.
; TITLE OF INVENTION: TRANSGENICALLY PRODUCED
; TITLE OF INVENTION: NON-SECRETED PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
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; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,551
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: TCI-046CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-028-551-7

Query Match 53.6%; Score 26.8; DB 4; Length 54;
Best Local Similarity 81.6%; Pred. No. 0.22;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGAACCTCTCATCTTACTGCTGTGGCTGCTGC 38
Db 12 ATGAAGTCTCATCTTACTGCTGTGGCTGCTGC 49

RESULT 15

US-09-028-551-8/c
; Sequence 8, Application US/09028551
; Patent No. 6528699
; GENERAL INFORMATION:
; APPLICANT: Harry Meade et al.
; TITLE OF INVENTION: TRANSGENICALLY PRODUCED
; TITLE OF INVENTION: NON-SECRETED PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,551
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: TCI-046CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 54 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-028-551-8

Query Match 53.6%; Score 26.8; DB 4; Length 54;
Best Local Similarity 81.6%; Pred. No. 0.22;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGAACCTCTCATCTTACTGCTGTGGCTGCTGC 38
Db 48 ATGAAGTCTCATCTTACTGCTGTGGCTGCTGC 11

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2005, 13:26:16 ; Search time 466.372 Seconds
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Title: US-10-820-777-2

Perfect score: 50

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	39	78.0	375	9	US-09-960-352-953
C 3	39	78.0	388	9	US-09-960-352-10691
C 4	39	78.0	390	9	US-09-960-352-9038
C 5	39	78.0	399	9	US-09-960-352-14946
C 6	39	78.0	408	9	US-09-960-352-5742
C 7	39	78.0	408	9	US-09-960-352-14242

C 8	39	78.0	411	9	US-09-960-352-9712	Sequence 9712, Ap
C 9	39	78.0	412	9	US-09-960-352-12606	Sequence 12606, A
C 10	39	78.0	413	9	US-09-960-352-4541	Sequence 4541, Ap
C 11	39	78.0	417	9	US-09-960-352-13070	Sequence 13070, A
C 12	39	78.0	428	9	US-09-960-352-4083	Sequence 4083, Ap
C 13	39	78.0	428	9	US-09-960-352-13294	Sequence 13294, A
C 14	39	78.0	432	9	US-09-960-352-304	Sequence 304, App
C 15	39	78.0	434	9	US-09-960-352-12097	Sequence 12097, A
C 16	39	78.0	435	9	US-09-960-352-1668	Sequence 1668, Ap
C 17	39	78.0	437	9	US-09-960-352-14237	Sequence 14237, A
C 18	39	78.0	440	9	US-09-960-352-741	Sequence 741, App
C 19	39	78.0	445	9	US-09-960-352-11394	Sequence 11394, A
C 20	39	78.0	450	9	US-09-960-352-712	Sequence 712, App
C 21	39	78.0	1123	8	US-08-545-573A-40	Sequence 40, Appl
C 22	37.4	74.8	89	13	US-10-079-623-333	Sequence 333, App
C 23	37.4	74.8	384	9	US-09-960-352-4568	Sequence 4568, Ap
C 24	37.4	74.8	413	9	US-09-960-352-9483	Sequence 9483, Ap
C 25	37.4	74.8	417	9	US-09-960-352-1673	Sequence 1673, Ap
C 26	37.4	74.8	420	9	US-09-960-352-761	Sequence 761, App
C 27	37.4	74.8	443	9	US-09-960-352-14939	Sequence 14939, A
C 28	35.8	71.6	51	16	US-10-170-221-37	Sequence 37, Appl
C 29	35.8	71.6	51	22	US-10-987-587-37	Sequence 37, Appl
C 30	32.8	65.6	471	9	US-09-960-352-5980	Sequence 5980, Ap
C 31	32.6	65.2	268	9	US-09-960-352-1901	Sequence 1901, Ap
C 32	32.6	65.2	415	9	US-09-960-352-8818	Sequence 8818, Ap
C 33	32.6	65.2	981	21	US-10-956-157-723	Sequence 723, App
C 34	32.6	65.2	981	21	US-10-956-157-723	Sequence 723, App
C 35	31.4	62.8	85	13	US-10-079-623-113	Sequence 113, App
C 36	31	62.0	349	9	US-09-960-352-2374	Sequence 2374, Ap
C 37	31	62.0	668	9	US-09-897-006-12	Sequence 12, Appl
C 38	31	62.0	668	10	US-09-897-511A-12	Sequence 12, Appl
C 39	31	62.0	668	17	US-10-397-079-12	Sequence 12, Appl
C 40	31	62.0	668	20	US-10-759-315-12	Sequence 12, Appl
C 41	31	62.0	668	21	US-10-947-881-12	Sequence 12, Appl
C 42	31	62.0	668	23	US-11-018-895-12	Sequence 12, Appl
C 43	30	60.0	588	24	US-11-097-143-31514	Sequence 31514, A
C 44	29	58.0	93	13	US-10-079-623-298	Sequence 298, App
C 45	27.8	55.6	752	17	US-10-085-198-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-09-960-352-12853/c

; Sequence 12853: Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing

; APPLICANT: Byatt, John C.

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

; FILE REFERENCE: 16511.006/37-21(10298)C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 12853

; LENGTH: 337

; TYPE: DNA

; ORGANISM: Bos taurus

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (32)

; OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: 55-LIB2809-027-Q1-E1-F4

US-09-960-352-12853

Query Match 78.0%; Score 39; DB 9; Length 337;

Best Local Similarity 100.0%; Pred. No. 3.3e-05;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 304 ATGAAACTTCTCATCTTACCTGCTTGTGGCTGTTGCT 266

RESULT 2

US-09-960-352-953/c
; Sequence 953, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 953
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 05-LIB188-007-Q1-E1-B9
US-09-960-352-953

Query Match 78.0%; Score 39; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACTTCTCATCTTACCTGCTTGTGGCTGTTGCT 39
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Db 368 ATGAAACTTCTCATCTTACCTGCTTGTGGCTGTTGCT 330

RESULT 3

US-09-960-352-10691
; Sequence 10691, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 10691
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 46-LIB2809-027-Q1-E1-D6
US-09-960-352-10691

Query Match 78.0%; Score 39; DB 9; Length 388;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACTTCTCATCTTACCTGCTTGTGGCTGTTGCT 39
|||||
Db 54 ATGAAACTTCTCATCTTACCTGCTTGTGGCTGTTGCT 92

RESULT 4

US-09-960-352-9038/c
; Sequence 9038, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9038
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB2809-013-Q1-E1-B12
US-09-960-352-9038

Query Match 78.0%; Score 39; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACTTCTCATCTTACCTGCTTGTGGCTGTTGCT 39
|||||
Db 341 ATGAAACTTCTCATCTTACCTGCTTGTGGCTGTTGCT 303

RESULT 5

US-09-960-352-14946/c
; Sequence 14946, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14946
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 64-LIB2809-027-Q1-E1-H8
US-09-960-352-14946

Query Match 78.0%; Score 39; DB 9; Length 399;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACTTCTCATCTTACCTGCTTGTGGCTGTTGCT 39
|||||
Db 353 ATGAAACTTCTCATCTTACCTGCTTGTGGCTGTTGCT 315

RESULT 6

US-09-960-352-5742/c
; Sequence 5742, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5742
; LENGTH: 408


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; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 25-LIB2809-002-Q1-E1-G1
US-09-960-352-5742

Query Match      78.0%; Score 39; DB 9; Length 408;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCTCATCCTTACCTGCTTGTGGCTGTGCT 39
    |||||
Db 362 ATGAACTTCTCATCCTTACCTGCTTGTGGCTGTGCT 324

RESULT 7
US-09-960-352-14242/c
; Sequence 14242, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14242
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 61-LIB2809-013-Q1-E1-H10
US-09-960-352-14242

Query Match      78.0%; Score 39; DB 9; Length 408;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCTCATCCTTACCTGCTTGTGGCTGTGCT 39
    |||||
Db 327 ATGAACTTCTCATCCTTACCTGCTTGTGGCTGTGCT 289

RESULT 8
US-09-960-352-9712
; Sequence 9712, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9712
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 42-LIB2809-010-Q1-E1-C6
US-09-960-352-9712

Query Match      78.0%; Score 39; DB 9; Length 411;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCTCATCCTTACCTGCTTGTGGCTGTGCT 39
    |||||
Db 362 ATGAACTTCTCATCCTTACCTGCTTGTGGCTGTGCT 324

RESULT 9
US-09-960-352-12606/c
; Sequence 12606, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12606
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 54-LIB2809-027-Q1-E1-F6
US-09-960-352-12606

Query Match      78.0%; Score 39; DB 9; Length 412;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCTCATCCTTACCTGCTTGTGGCTGTGCT 39
    |||||
Db 367 ATGAACTTCTCATCCTTACCTGCTTGTGGCTGTGCT 329

RESULT 10
US-09-960-352-4541/c
; Sequence 4541, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4541
; LENGTH: 413
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB2809-001-Q1-E1-E7
US-09-960-352-4541

Query Match      78.0%; Score 39; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACTTCTCATCCTTACCTGCTTGTGGCTGTGCT 39
    |||||
Db 362 ATGAACTTCTCATCCTTACCTGCTTGTGGCTGTGCT 324

RESULT 11
US-09-960-352-13070/c
; Sequence 13070, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
```

; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 13070
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 56-LIB2809-013-Q1-E1-F8
US-09-960-352-13070

Query Match 78.0%; Score 39; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTCATCCTTACCTGCTGTTGGCTGTTGCT 39
|||||
Db 362 ATGAAACTTCTCATCCTTACCTGCTGTTGGCTGTTGCT 324

RESULT 12
US-09-960-352-4083/C
; Sequence 4083, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4083
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 18-LIB2809-024-Q1-E1-E5
US-09-960-352-4083

Query Match 78.0%; Score 39; DB 9; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTCATCCTTACCTGCTGTTGGCTGTTGCT 39
|||||
Db 393 ATGAAACTTCTCATCCTTACCTGCTGTTGGCTGTTGCT 355

RESULT 13
US-09-960-352-13294
; Sequence 13294, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 13294
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 57-LIB2809-005-Q1-E1-G2
US-09-960-352-13294

Query Match 78.0%; Score 39; DB 9; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTCATCCTTACCTGCTGTTGGCTGTTGCT 39
|||||
Db 185 ATGAAACTTCTCATCCTTACCTGCTGTTGGCTGTTGCT 223

RESULT 14
US-09-960-352-304/C
; Sequence 304, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 304
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 02-LIB2809-032-Q1-E1-A5
US-09-960-352-304

Query Match 78.0%; Score 39; DB 9; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTCATCCTTACCTGCTGTTGGCTGTTGCT 39
|||||
Db 377 ATGAAACTTCTCATCCTTACCTGCTGTTGGCTGTTGCT 339

RESULT 15
US-09-960-352-12097/C
; Sequence 12097, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12097
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 52-LIB188-014-Q1-E1-E12
US-09-960-352-12097

Query Match 78.0%; Score 39; DB 9; Length 434;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACTTCTCATCCTTACCTGCTGTTGGCTGTTGCT 39
|||||
Db 367 ATGAAACTTCTCATCCTTACCTGCTGTTGGCTGTTGCT 329

Search completed: October 1, 2005, 15:58:56
Job time : 466.372 secs

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